



#5

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Fig.1.

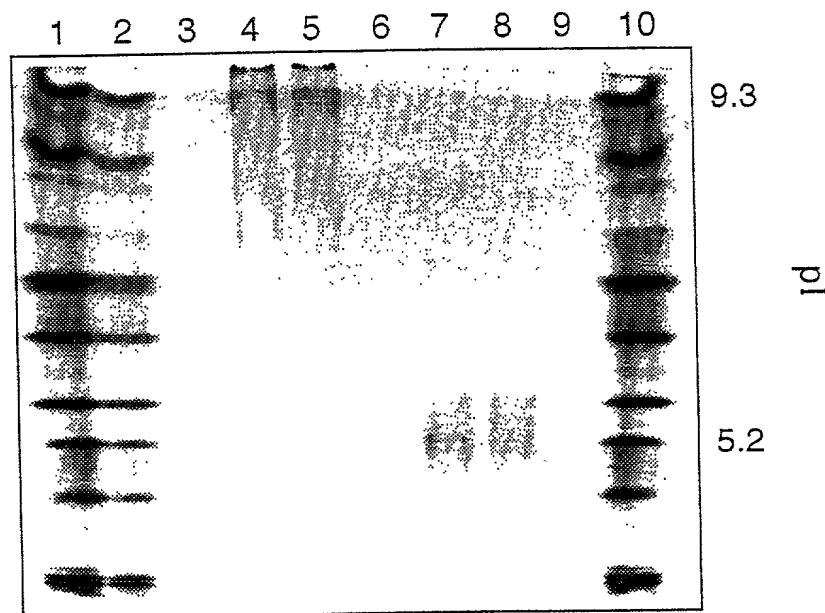


Fig.2.

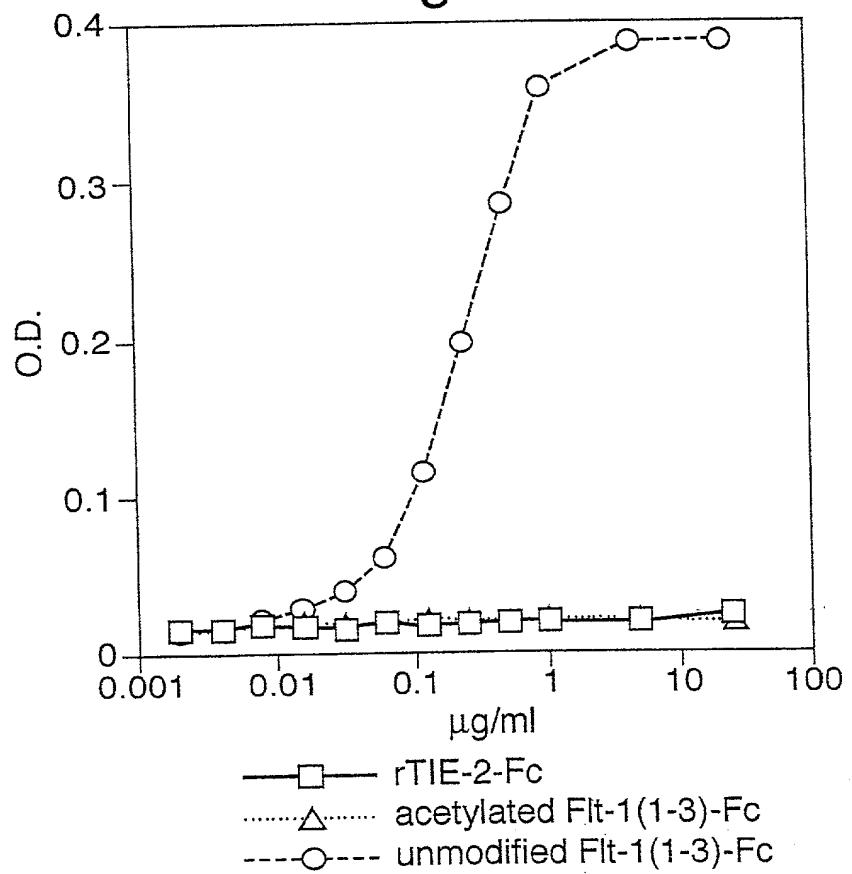




Fig.3.

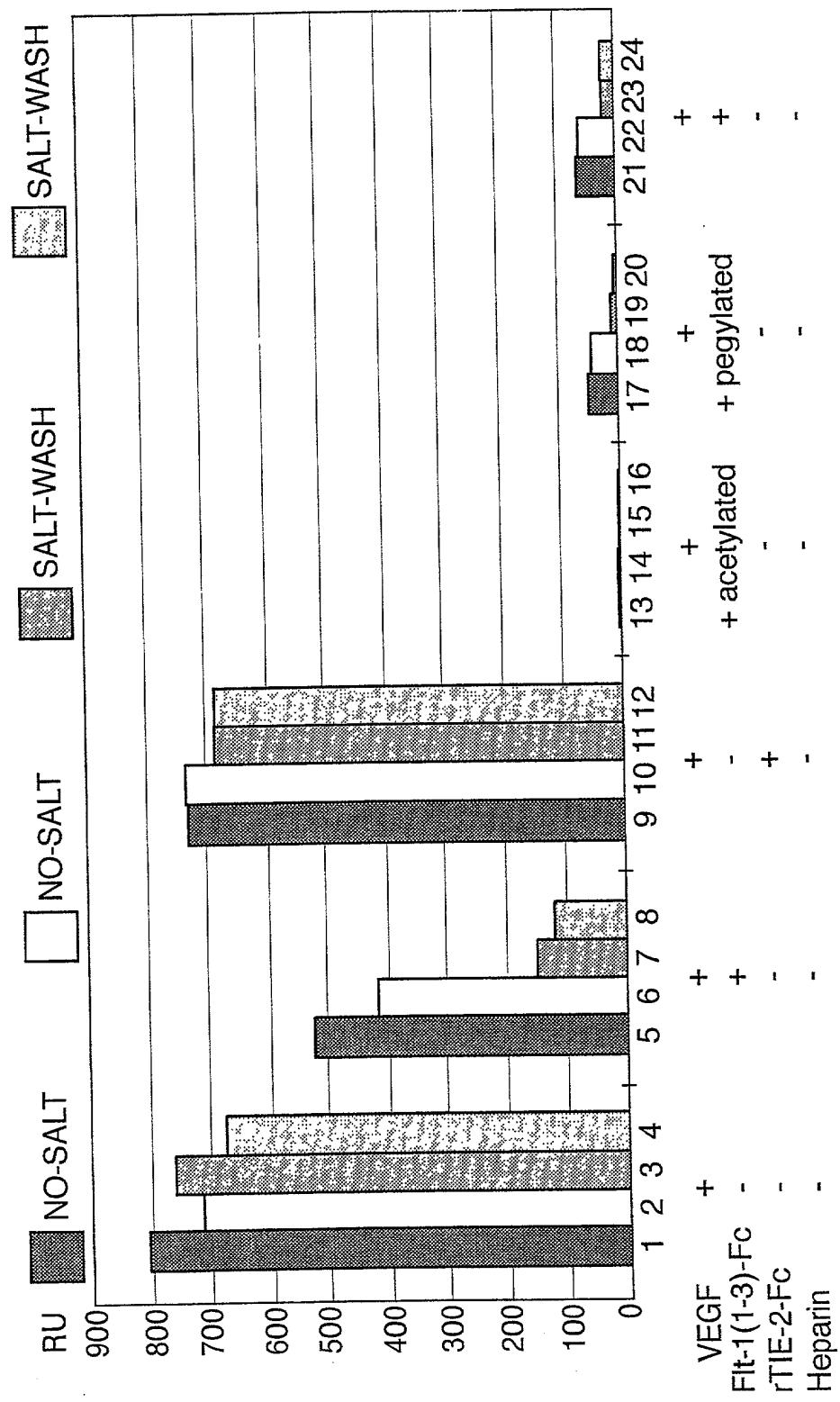


Fig.4.

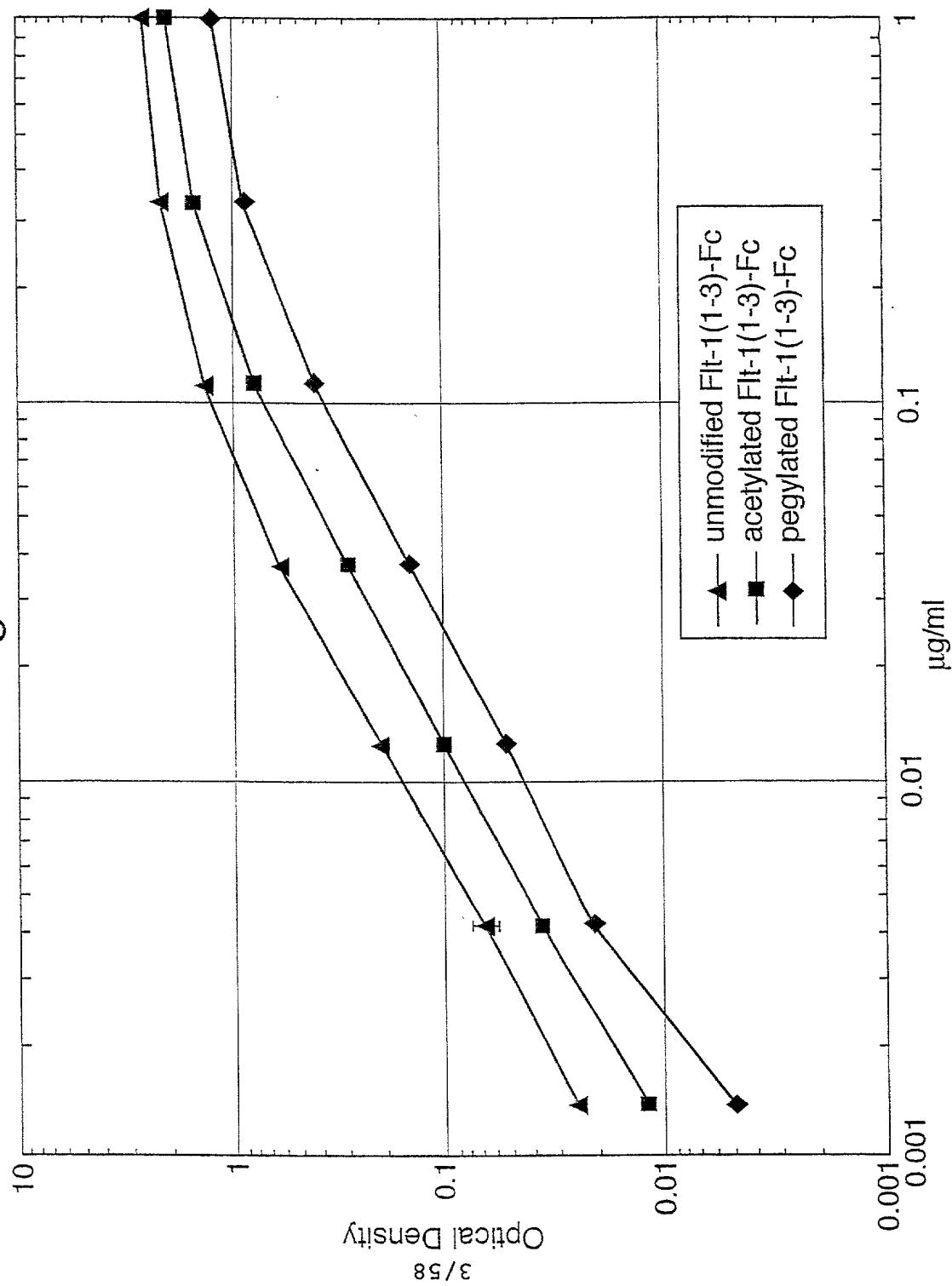
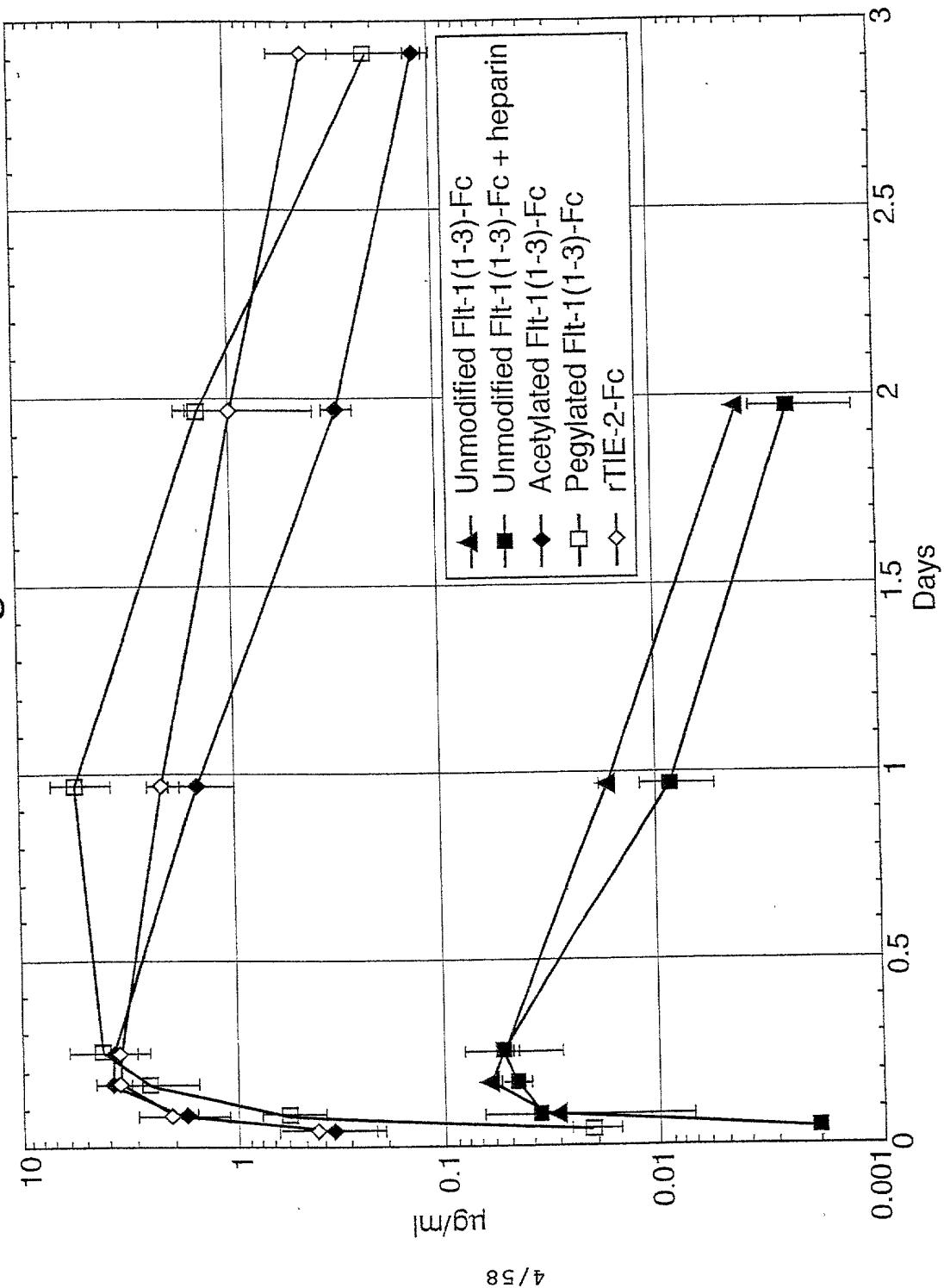
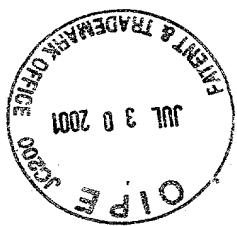


Fig. 5.



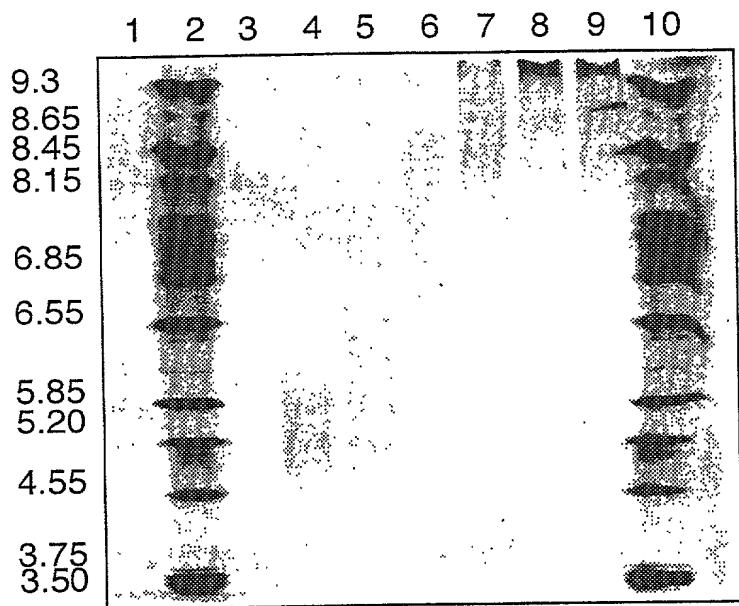
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Fig.6A.



TELECO INC. 2000

Fig.6B.

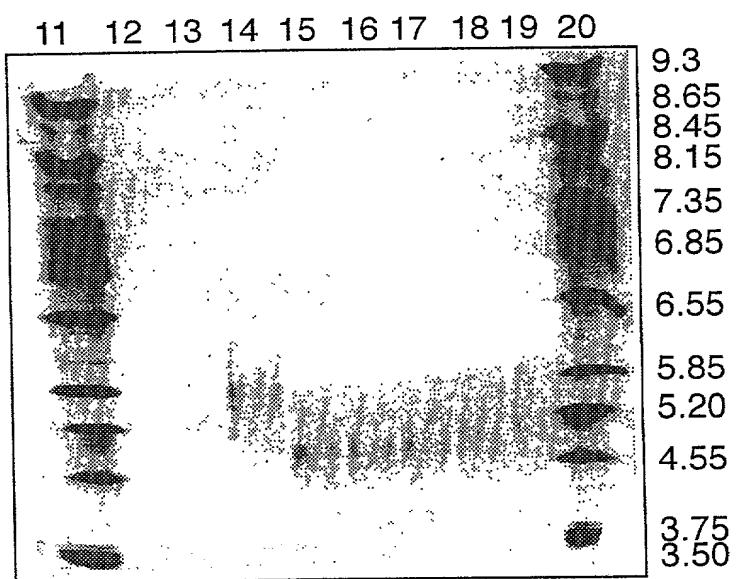




Fig.7.

PCT/US2000/012560

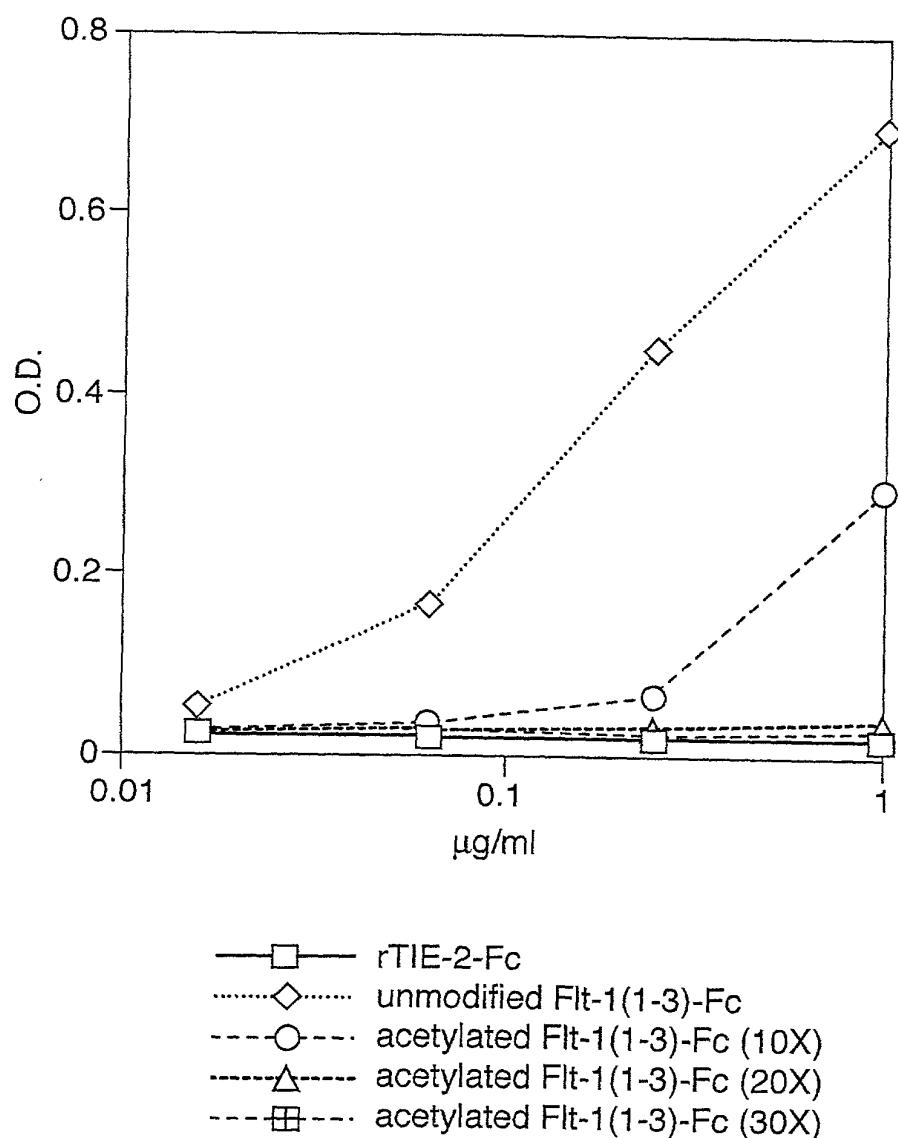




Fig. 8.

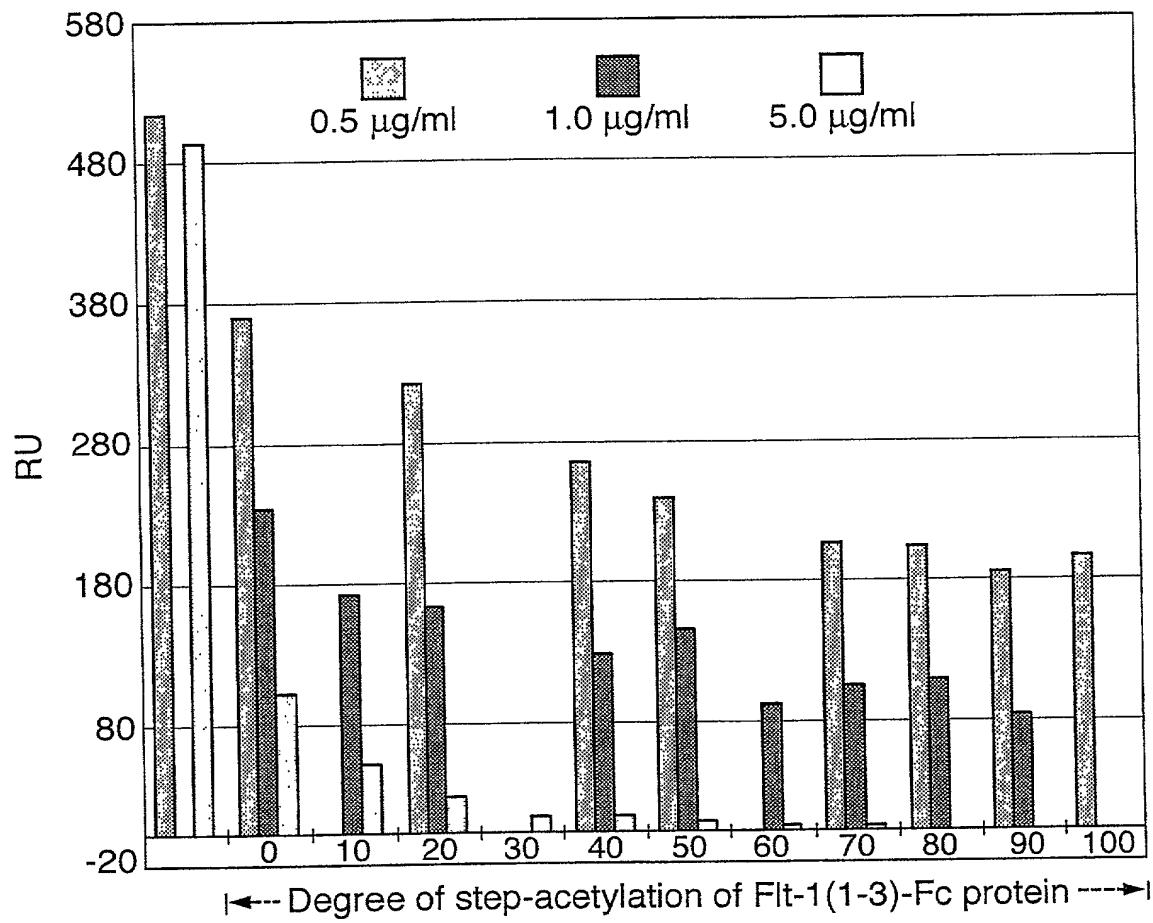


Fig. 9.

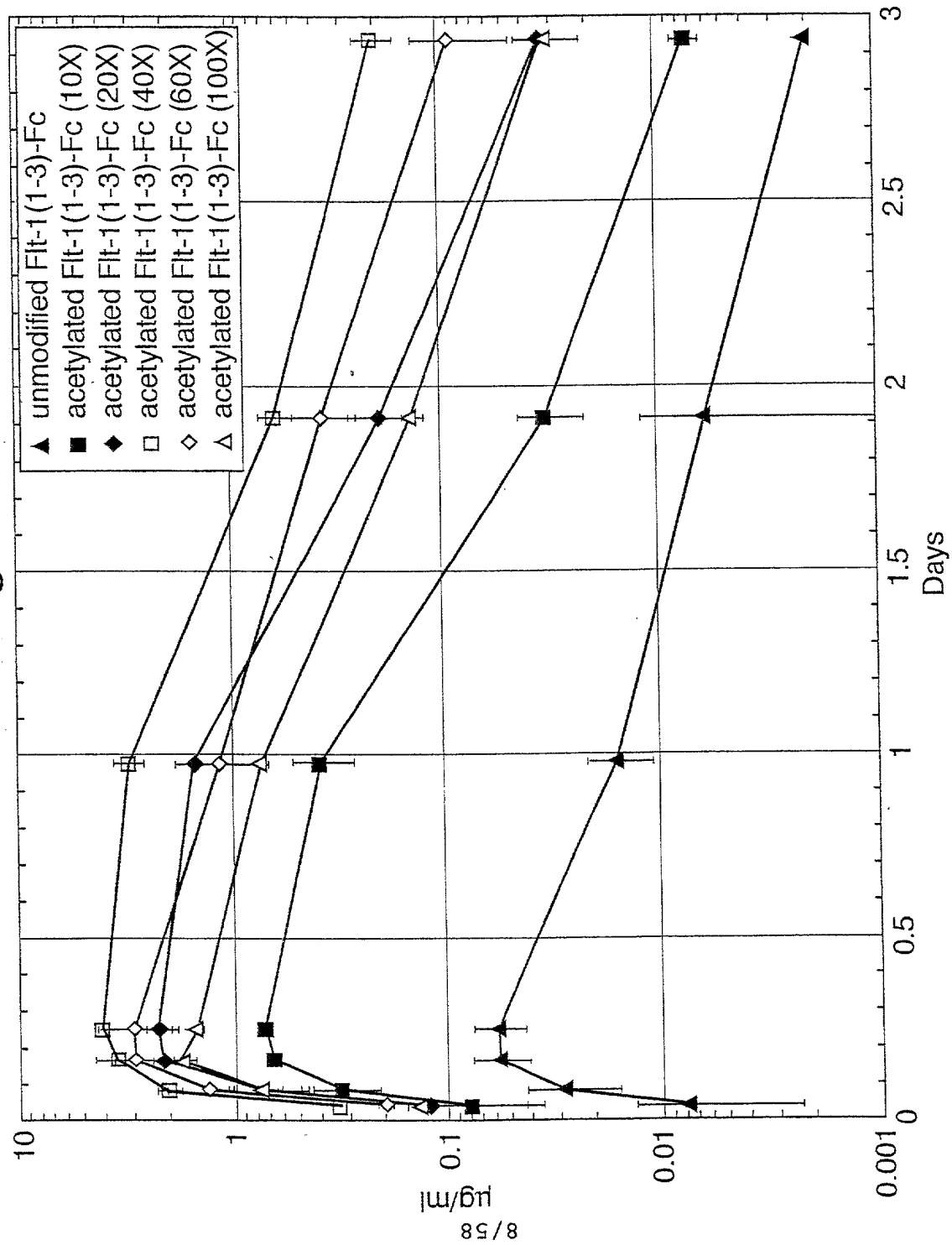




Fig. 10A.

ATG GTC AGC TAC TGG GAC ACC GGG GTC CTG CTG TGC GCG CTG CTC AGC TGT CTG CTT CTC
 TAC CAG TCG ATG ACC CTG TGG CCC CAG GAC ACG CGC GAC GAG TCG ACA GAC GAA GAG
 Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser Cys Leu Leu Leu>

 ACA GGA TCT AGT TCA GGT TCA AAA TTA AAA GAT CCT GAA CTG AGT TTA AAA GGC ACC CAG
 TGT CCT AGA TCA AGT CCA AGT TTT AAT TTT CTA GGA CTT GAC TCA AAT TTT CCG TGG GTC
 Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro Glu Leu Ser Leu Lys Gly Thr Gln>

 CAC ATC ATG CAA GCA GGC CAG ACA CTG CAT CTC CAA TGC AGG GGG GAA GCA GCC CAT AAA
 GTG TAG TAC GTT CGT CCG GTC TGT GAC GTA GAG GTT ACG TCC CCC CTT CGT CGG GTA TTT
 His Ile Met Gln Ala Gly Gln Thr Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys>

 TGG TCT TTG CCT GAA ATG GTG AGT AAG GAA AGC GAA AGG CTG AGC ATA ACT AAA TCT GCC
 ACC AGA AAC GGA CTT TAC CAC TCA TTC CTT TCG CTT TCC GAC TCG TAT TGA TTT AGA CGG
 Trp Ser Leu Pro Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala>

 TGT GGA AGA AAT GGC AAA CAA TTC TGC AGT ACT TTA ACC TTG AAC ACA GCT CAA GCA AAC
 ACA CCT TCT TTA CCG TTT GTT AAG ACG TCA TGA AAT TGG AAC TTG TGT CGA GTT CGT TTG
 Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr Ala Gln Ala Asn>

 CAC ACT GGC TTC TAC AGC TGC AAA TAT CTA GCT GTA CCT ACT TCA AAG AAG AAG GAA ACA
 GTG TGA CCG AAG ATG TCG ACG TTT ATA GAT CGA CAT GGA TGA AGT TTC TTC TCC CTT TGT
 His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val Pro Thr Ser Lys Lys Glu Thr>

 GAA TCT GCA ATC TAT ATA TTT ATT AGT GAT ACA GGT AGA CCT TTC GTA GAG ATG TAC AGT
 CTT AGA CGT TAG ATA TAT AAA TAA TCA CTA TGT CCA TCT GGA AAG CAT CTC TAC ATG TCA
 Glu Ser Ala Ile Tyr Ile Phe Ile Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser>

 GAA ATC CCC GAA ATT ATA CAC ATG ACT GAA GGA AGG GAG CTC GTC ATT CCC TGC CGG GTT
 CTT TAG GGG CTT TAA TAT GTG TAC TGA CTT CCT TCC CTC GAG CAG TAA GGG ACG GCC CAA
 Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val>

 ACG TCA CCT AAC ATC ACT GTT ACT TTA AAA AAG TTT CCA CTT GAC ACT TTG ATC CCT GAT
 TGC AGT GGA TTG TAG TGA CAA TGA AAT TTT TTC AAA GGT GAA CTG TGA AAC TAG GGA CTA
 Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp>



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Fig.10B.

550 560 570 580 590 600
 * * * * * * * * * * * * *
 GGA AAA CGC ATA ATC TGG GAC AGT AGA AAG GGC TTC ATC ATA TCA AAT GCA ACG TAC AAA
 CCT TTT GCG TAT TAG ACC CTG TCA TCT TTC CCG AAG TAG TAT AGT TTA CGT TGC ATG TTT
 Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys>

 610 620 630 640 650 660
 * * * * * * * * * * * *
 GAA ATA GGG CTT CTG ACC TGT GAA GCA ACA GTC AAT GGG CAT TTG TAT AAG ACA AAC TAT
 CTT TAT CCC GAA GAC TGG ACA CTT CGT TGT CAG TTA CCC GTC AAC ATA TTC TGT TTG ATA
 Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr>

 670 680 690 700 710 720
 * * * * * * * * * * * *
 CTC ACA CAT CGA CAA ACC AAT ACA ATC ATA GAT GTC CAA ATA AGC ACA CCA CGC CCA GTC
 GAG TGT GTA GCT GTT TGG TTA TGT TAG TAT CTA CAG GTT TAT TCG TGT GGT GCG GGT CAG
 Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val>

 730 740 750 760 770 780
 * * * * * * * * * * * *
 AAA TTA CTT AGA GGC CAT ACT CTT GTC CTC AAT TGT ACT GCT ACC ACT CCC TTG AAC ACG
 TTT AAT GAA TCT CCG GTA TGA GAA CAG GAG TTA ACA TGA CGA TGG TGA GGG AAC TTG TGC
 Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr>

 790 800 810 820 830 840
 * * * * * * * * * * * *
 AGA GTT CAA ATG ACC TGG AGT TAC CCT GAT GAA AAA AAT AAG AGA GCT TCC GTA AGG CGA
 TCT CAA GTT TAC TGG ACC TCA ATG GGA CTA CTT TTT TTA TTC TCT CGA AGG CAT TCC GCT
 Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Lys Asn Lys Arg Ala Ser Val Arg Arg>

 850 860 870 880 890 900
 * * * * * * * * * * * *
 CGA ATT GAC CAA AGC AAT TCC CAT GCC AAC ATA TTC TAC AGT GTT CTT ACT ATT GAC AAA
 GCT TAA CTG GTT TCG TTA AGG GTA CGG TTG TAT AAG ATG TCA CAA GAA TGA TAA CTG TTT
 Arg Ile Asp Gln Ser Asn Ser His Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys>

 910 920 930 940 950 960
 * * * * * * * * * * * *
 ATG CAG AAC AAA GAC AAA GGA CTT TAT ACT TGT CGT GTA AGG AGT GGA CCA TCA TTC AAA
 TAC GTC TTG TTT CTG TTT CCT GAA ATA TGA ACA GCA CAT TCC TCA CCT GGT AGT AAG TTT
 Met Gln Asn Lys Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys>

 970 980 990 1000 1010 1020
 * * * * * * * * * * * *
 TCT GTT AAC ACC TCA GTG CAT ATA TAT GAT AAA GCA GGC CCG GGC GAG CCC AAA TCT TGT
 AGA CAA TTG TGG AGT CAC GTA TAT ATA CTA TTT CGT CCG GGC CCG CTC GGG TTT AGA ACA
 Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Gly Pro Gly Glu Pro Lys Ser Cys>

 1030 1040 1050 1060 1070 1080
 * * * * * * * * * * * *
 GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC
 CTG TTT TGA GTG TGT ACG GGT GGC ACG GGT CGT GGA CTT GAG GAC CCC CCT GGC AGT CAG
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Pro Ser Val>

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Fig. 10C.



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Fig.10D.

1630 1640 1650 1660 1670 1680
* * * * * * *
AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC
TTG CAG AAG AGT ACG AGG CAC TAC GTA CTC CGA GAC GTG TGT GTG ATG TGC GTC TTC TCG
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser>

1690 1700
* * * *
CTC TCC CTG TCT CCG GGT AAA TGA
GAG AGG GAC AGA GGC CCA TTT ACT
Leu Ser Leu Ser Pro Gly Lys ***>

12/58 100% 225% 300% 400%

Fig. 11.

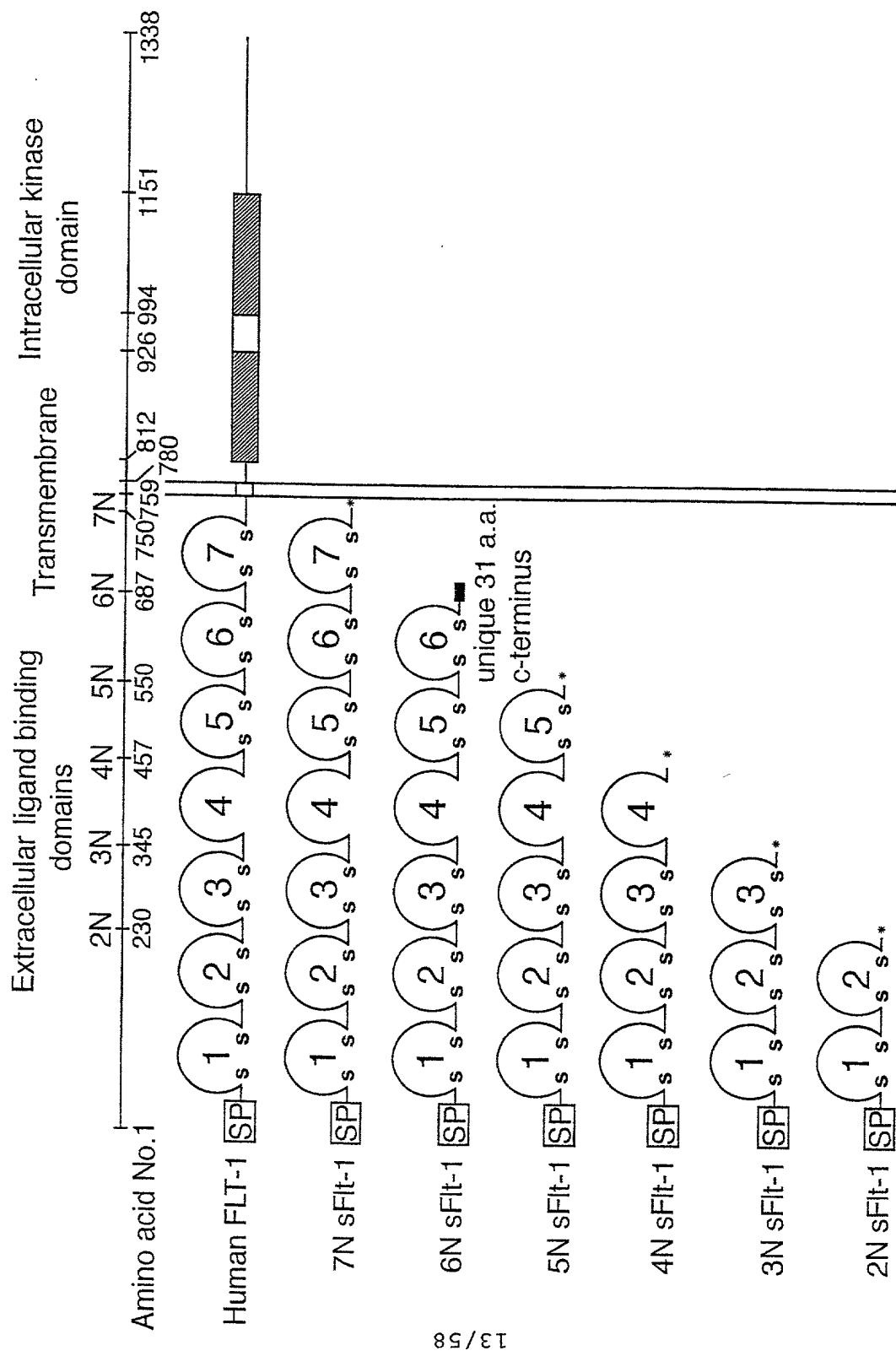
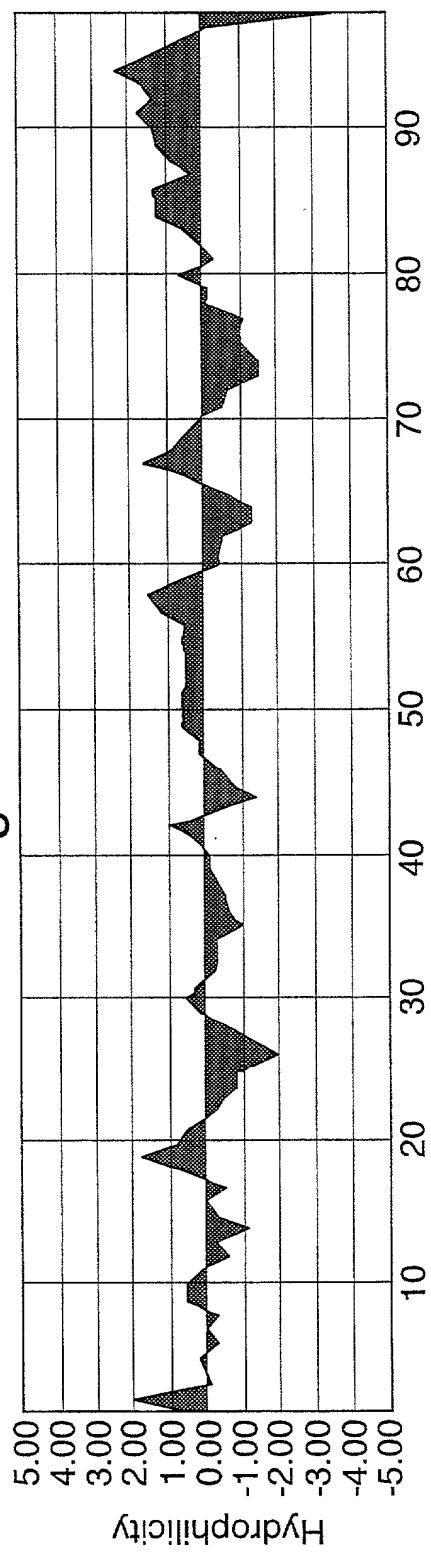


Fig.12A.



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Fig.12B.

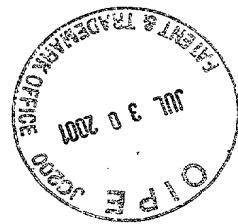
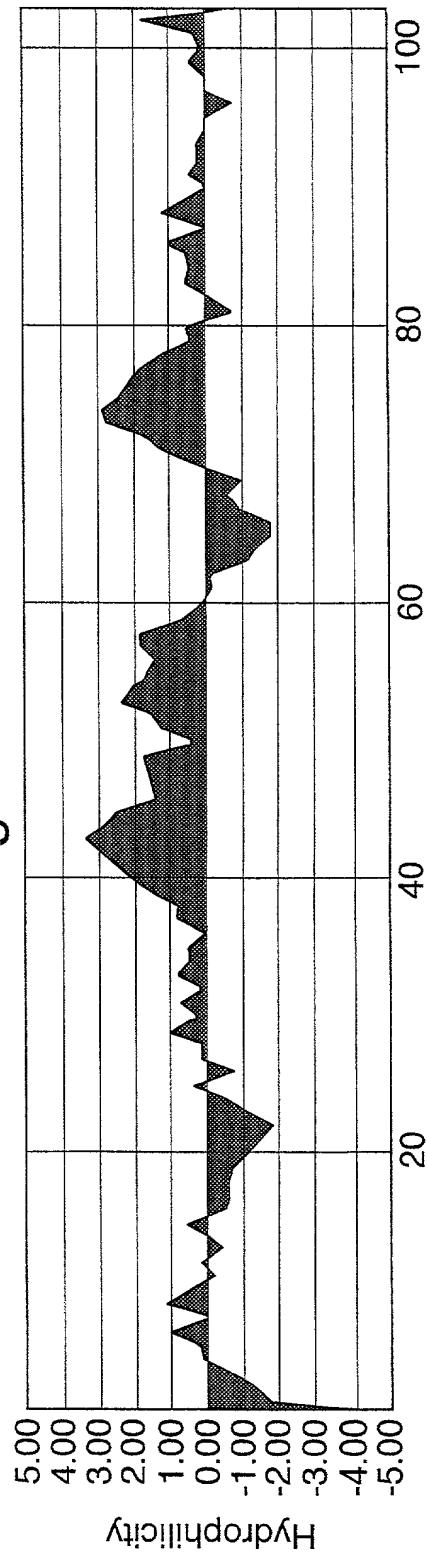




Fig. 13A.



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Fig.13B.

550 560 570 580 590 600

* * * * * *

GGA AAA CGC ATA ATC TGG GAC AGT AGA AAG GGC TTC ATC ATA TCA AAT GCA ACG TAC AAA
CCT TTT GCG TAT TAG ACC CTG TCA TCT TTC CCG AAG TAG TAT AGT TTA CGT TGC ATG TTT
Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys>

610 620 630 640 650 660

* * * * * *

GAA ATA GGG CTT CTG ACC TGT GAA GCA ACA GTC AAT GGG CAT TTG TAT AAG ACA AAC TAT
CTT TAT CCC GAA GAC TGG ACA CTT CGT TGT CAG TTA CCC GTA AAC ATA TTC TGT TTG ATA
Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr>

670 680 690 700 710 720

* * * * * *

CTC ACA CAT CGA CAA ACC AAT ACA ATC ATA GAT GTC CAA ATA AGC ACA CCA CGC CCA GTC
GAG TGT GTA GCT GTT TGG TTA TGT TAG TAT CTA CAG GTT TAT TCG TGT GGT GCG GGT CAG
Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val>

730 740 750 760 770 780

* * * * * *

AAA TTA CTT AGA GGC CAT ACT CTT GTC CTC AAT TGT ACT GCT ACC ACT CCC TTG AAC ACG
TTT AAT GAA TCT CCG GTA TGA GAA CAG TTA ACA TGA CGA TGG TGA GGG AAC TTG TGC
Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Pro Leu Asn Thr>

790 800 810 820 830 840

* * * * * *

AGA GTT CAA ATG ACC TGG AGT TAC CCT GAT GAA ATT GAC CAA AGC AAT TCC CAT GCC AAC
TCT CAA GTT TAC TGG ACC TCA ATG GGA CTA CTT TAA CTG GTT TCG TTA AGG GTA CGG TTG
Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Ile Asp Gln Ser Asn Ser His Ala Asn>

850 860 870 880 890 900

* * * * * *

ATA TTC TAC AGT GTT CTT ACT ATT GAC AAA ATG CAG AAC AAA GAC AAA GGA CTT TAT ACT
TAT AAG ATG TCA CAA GAA TGA TAA CTG TTT TAC GTC TTG TTT CTG TTT CCT GAA ATA TGA
Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys Asp Lys Gly Leu Tyr Thr>

910 920 930 940 950 960

* * * * * *

TGT CGT GTA AGG AGT GGA CCA TCA TTC AAA TCT GTT AAC ACC TCA GTG CAT ATA TAT GAT
ACA GCA CAT TCC TCA CCT GGT AGT AAG TTT AGA CAA TTG TGG AGT CAC GTA TAT ATA CTA
Cys Arg Val Arg Ser Gly Pro Ser Phe Lys Ser Val Asn Thr Ser Val His Ile Tyr Asp>

970 980 990 1000 1010 1020

* * * * * *

AAA GCA GGC CCG GGC GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA
TTT CGT CCG GGC CCG CTC GGG TTT AGA ACA CTG TTT TGA GTG TGT ACG GGT GGC ACG GGT
Lys Ala Gly Pro Gly Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro>

1030 1040 1050 1060 1070 1080

* * * * * *

GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC CCC CCA AAA CCC AAG GAC ACC
CGT GGA CTT GAG GAC CCC CCT GGC AGT CAG AAG GAG AAG GGG GGT TTT GGG TTC CTG TGG
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr>



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Fig. 13C.



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Fig.13D.

1630 1640 1650 1660 1670

* * * * *

GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA TGA
CGA GAC GTG TTG GTG ATG TGC GTC TTC TCG GAG AGG GAC AGA GGC CCA TTT ACT
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys ***>

TOP SECRET//COMINT



Fig. 14A.

10	20	30	40	50	60
*	*	*	*	*	*
ATG GTC AGC TAC TGG GAC ACC GGG GTC CTG CTG TGC GCG CTG CTC AGC TGT CTG CTT CTC	TAC CAG TCG ATG ACC CTG TGG CCC CAG GAC GAC ACG CGC GAC GAG TCG ACA GAC GAA GAG	Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser Cys Leu Leu Leu>			
70	80	90	100	110	120
*	*	*	*	*	*
ACA GGA TCT AGT TCC GGA GGT AGA CCT TTC GTA GAG ATG TAC AGT GAA ATC CCC GAA ATT	TGT CCT AGA TCA AGG CCT CCA TCT GGA AAG CAT CTC TAC ATG TCA CTT TAG GGG CTT TAA	Thr Gly Ser Ser Ser Gly Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu Ile>			
130	140	150	160	170	180
*	*	*	*	*	*
ATA CAC ATG ACT GAA GGA AGG GAG CTC GTC ATT CCC TGC CGG GTT ACG TCA CCT AAC ATC	TAT GTG TAC TGA CTT CCT CTC GAG CAG TAA GGG ACG GCC CAA TGC AGT GGA TTG TAG	Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile>			
190	200	210	220	230	240
*	*	*	*	*	*
ACT GTT ACT TTA AAA AAG TTT CCA CTT GAC ACT TTG ATC CCT GAT GGA AAA CGC ATA ATC	TGA CAA TGA AAT TTT TTC AAA GGT GAA CTG TGA AAC TAG GGA CTA CCT TTT GCG TAT TAG	Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile>			
250	260	270	280	290	300
*	*	*	*	*	*
TGG GAC AGT AGA AAG GGC TTC ATC ATA TCA AAT GCA ACG TAC AAA GAA ATA GGG CTT CTG	ACC CTG TCA TCT TTC CCG AAG TAG TAT AGT TTA CGT TGC ATG TTT CTT TAT CCC GAA GAC	Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu>			
310	320	330	340	350	360
*	*	*	*	*	*
ACC TGT GAA GCA ACA GTC AAT GGG CAT TTG TAT AAG ACA AAC TAT CTC ACA CAT CGA CAA	TGG ACA CTT CGT TGT CAG TTA CCC GTA AAC ATA TTC TGT TTG ATA GAG TGT GTA GCT GTT	Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln>			
370	380	390	400	410	420
*	*	*	*	*	*
ACC AAT ACA ATC ATA GAT GTC CAA ATA AGC ACA CCA CGC CCA GTC AAA TTA CTT AGA GGC	TGG TTA TGT TAG TAT CTA CAG GTT TAT TCG TGT GGT GCG GGT CAG TTT AAT GAA TCT CCG	Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val Lys Leu Leu Arg Gly>			
430	440	450	460	470	480
*	*	*	*	*	*
CAT ACT CTT GTC CTC AAT TGT ACT GCT ACC ACT CCC TTG AAC ACG AGA GTT CAA ATG ACC	GTA TGA GAA CAG GAG TTA ACA TGA CGA TGG TGA GGG AAC TTG TGC TCT CAA GTT TAC TGG	His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr Arg Val Gln Met Thr>			
490	500	510	520	530	540
*	*	*	*	*	*
TGG AGT TAC CCT GAT GAA ATT GAC CAA AGC AAT TCC CAT GCC AAC ATA TTC TAC AGT GTT	ACC TCA ATG GGA CTA CTT TAA CTG GTT TCG TTA AGG GTA CGG TTG TAT AAG ATG TCA CAA	Trp Ser Tyr Pro Asp Glu Ile Asp Gln Ser Asn Ser His Ala Asn Ile Phe Tyr Ser Val>			



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Fig.14B.

550 560 570 580 590 600

* * * * * * *

CTT ACT ATT GAC AAA ATG CAG AAC AAA GAC AAA GGA CTT TAT ACT TGT CGT GTA AGG AGT
GAA TGA TAA CTG TTT TAC GTC TTG CCT GAA ATA TGA ACA GCA CAT TCC TCA
Leu Thr Ile Asp Lys Met Gln Asn Lys Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser>

610 620 630 640 650 660

* * * * * * *

GGA CCA TCA TTC AAA TCT GTT AAC ACC TCA GTG CAT ATA TAT GAT AAA GCA GGC CCG GGC
CCT GGT AGT AAG TTT AGA CAA TTG TGG AGT CAC GTA TAT ATA CTA TTT CGT CCG GGC CCG
Gly Pro Ser Phe Lys Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Gly Pro Gly>

670 680 690 700 710 720

* * * * * * *

GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG
CTC GGG TTT AGA ACA CTG TTT TGA GTG TGT ACG GGT GGC ACG GGT CGT GGA CTT GAG GAC
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu>

730 740 750 760 770 780

* * * * * * *

GGG GGA CCG TCA GTC TTC CTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG
CCC CCT GGC AGT CAG AAG GAG AAG GGG GGT TTT GGG TTC CTG TGG GAG TAC TAG AGG GCC
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg>

790 800 810 820 830 840

* * * * * * *

ACC CCT GAG GTC ACA TGC GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC
TGG GGA CTC CAG TGT ACG CAC CAC CTG CAC TCG GTG CTT CTG GGA CTC CAG TTC AAG
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe>

850 860 870 880 890 900

* * * * * * *

AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG
TTG ACC ATG CAC CTG CCG CAC CTC CAC GTC TTA CGG TTC TGT TTC GGC GCC CTC CTC GTC
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln>

910 920 930 940 950 960

* * * * * * *

TAC AAC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT
ATG TTG TCG TGC ATG GCA CAC CAG TCG CAG GAG TGG CAG GAC GTG GTC CTG ACC GAC TTA
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn>

970 980 990 1000 1010 1020

* * * * * * *

GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GGC CTC CCA GCC CCC ATC GAG AAA ACC
CCG TTC CTC ATG TTC ACG TTC CAG AGG TTG TTT CGG GAG GGT CGG GGG TAG CTC TTT TGG
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr>

1030 1040 1050 1060 1070 1080

* * * * * * *

ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG
TAG AGG TTT CGG TTT CCC GTC GGG GCT CTT GGT GTC CAC ATG TGG GAC GGG GGT AGG GCC
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg>

FIGURE 14B



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Fig.14C.

1090 1100 1110 1120 1130 1140
 * * * * * * * *
 GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC
 CTA CTC GAC TGG TTC TTG GTC CAG TCG GAC TGG ACG GAC CAG TTT CCG AAG ATA GGG TCG
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser>

 1150 1160 1170 1180 1190 1200
 * * * * * * * *
 GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT
 CTG TAG CGG CAC CTC ACC CTC TCG TTA CCC GTC GGC CTC TTG TTG ATG TTC TGG TGC GGA
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro>

 1210 1220 1230 1240 1250 1260
 * * * * * * * * *
 CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC
 GGG CAC GAC CTG AGG CTG CCG AGG AAG AAG GAG ATG TCG TTC GAG TGG CAC CTG TTC TCG
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser>

 1270 1280 1290 1300 1310 1320
 * * * * * * * *
 AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC
 TCC ACC GTC GTC CCC TTG CAG AAG AGT ACG AGG CAC TAC GTA CTC CGA GAC GTG TTG GTG
 Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His>

 1330 1340 1350
 * * * * * * *
 TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA TGA
 ATG TGC GTC TTC TCG GAG AGG GAC AGA GGC CCA TTT ACT
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys ***>

FIGURE 14C



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Fig.15A.

10 20 30 40 50 60

* * * * * *

ATG GTC AGC TAC TGG GAC ACC GGG GTC CTG CTG TGC GCG CTG CTC AGC TGT CTG CTT CTC
TAC CAG TCG ATG ACC CTG TGG CCC CAG GAC GAC ACG CGC GAC GAG TCG ACA GAC GAA GAG
Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser Cys Leu Leu Leu>

70 80 90 100 110 120

* * * * * *

ACA GGA TCT AGT TCC GGA GGT AGA CCT TTC GTA GAG ATG TAC AGT GAA ATC CCC GAA ATT
TGT CCT AGA TCA AGG CCT CCA TCT GGA AAG CAT CTC TAC ATG TCA CTT TAG GGG CTT TAA
Thr Gly Ser Ser Gly Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu Ile>

130 140 150 160 170 180

* * * * * *

ATA CAC ATG ACT GAA GGA AGG GAG CTC GTC ATT CCC TGC CGG GTT ACG TCA CCT AAC ATC
TAT GTG TAC TGA CTT CCT TCC CTC GAG CAG TAA GGG ACG GCC CAA TGC AGT GGA TTG TAG
Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile>

190 200 210 220 230 240

* * * * * *

ACT GTT ACT TTA AAA AAG TTT CCA CTT GAC ACT TTG ATC CCT GAT GGA AAA CGC ATA ATC
TGA CAA TGA AAT TTT TTC AAA GGT GAA CTG TGA AAC TAG GGA CTA CCT TTT GCG TAT TAG
Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile>

250 260 270 280 290 300

* * * * * *

TGG GAC AGT AGA AAG GGC TTC ATC ATA TCA AAT GCA ACG TAC AAA GAA ATA GGG CTT CTG
ACC CTG TCA TCT TTC CCG AAG TAG TAT AGT TTA CGT TGC ATG TTT CTT TAT CCC GAA GAC
Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu>

310 320 330 340 350 360

* * * * * *

ACC TGT GAA GCA ACA GTC AAT GGG CAT TTG TAT AAG ACA AAC TAT CTC ACA CAT CGA CAA
TGG ACA CTT CGT TGT CAG TTA CCC GTA AAC ATA TTC TGT TTG ATA GAG TGT GTA GCT GTT
Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln>

370 380 390 400 410 420

* * * * * *

ACC AAT ACA ATA GAT GTC CAA ATA AGC ACA CCA CGC CCA GTC AAA TTA CTT AGA GGC
TGG TTA TGT TAG TAT CTA CAG GTT TAT TCG TGT GGT GCG GGT CAG TTT AAT GAA TCT CCG
Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val Lys Leu Arg Gly>

430 440 450 460 470 480

* * * * * *

CAT ACT CTT GTC CTC AAT TGT ACT GCT ACC ACT CCC TTG AAC ACG AGA GTT CAA ATG ACC
GTA TGA GAA CAG GAG TTA ACA TGA CGA TGG TGA GGG AAC TTG TGC TCT CAA GTT TAC TGG
His Thr Leu Val Leu Asn Cys Thr Ala Thr Pro Leu Asn Thr Arg Val Gln Met Thr>

490 500 510 520 530 540

* * * * * *

TGG AGT TAC CCT GAT GAA AAA AAT AAG AGA GCT TCC GTA AGG CGA CGA ATT GAC CAA AGC
ACC TCA ATG GGA CTA CTT TTT TTA TTC TCT CGA AGG CAT TCC GCT GCT TAA CTG GTT TCG
Trp Ser Tyr Pro Asp Glu Lys Asn Lys Arg Ala Ser Val Arg Arg Arg Ile Asp Gln Ser>



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Fig.15B.

550 560 570 580 590 600

* * * * * *

AAT TCC CAT GCC AAC ATA TTC TAC AGT GTT CTT ACT ATT GAC AAA ATG CAG AAC AAA GAC
TTA AGG GTA CGG TTG TAT AAG ATG TCA CAA GAA TGA TAA CTG TTT TAC GTC TTG TTT CTG
Asn Ser His Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys Asp>

610 620 630 640 650 660

* * * * * *

AAA GGA CTT TAT ACT TGT CGT GTA AGG AGT GGA CCA TCA TTC AAA TCT GTT AAC ACC TCA
TTT CCT GAA ATA TGA ACA GCA CAT TCC TCA CCT GGT AGT AAG TTT AGA CAA TTG TGG AGT
Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys Ser Val Asn Thr Ser>

670 680 690 700 710 720

* * * * * *

GTG CAT ATA TAT GAT AAA GCA GGC CCG GGC GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA
CAC GTA TAT ATA CTA TTT CGT CCG GGC CCG CTC GGG TTT AGA ACA CTG TTT TGA GTG TGT
Val His Ile Tyr Asp Lys Ala Gly Pro Glu Pro Lys Ser Cys Asp Lys Thr His Thr>

730 740 750 760 770 780

* * * * * *

TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA
ACG GGT GGC ACG GGT CGT GGA CTT GAG GAC CCC CCT GGC AGT CAG AAG GAG AAG GGG GGT
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Pro Ser Val Phe Leu Phe Pro Pro>

790 800 810 820 830 840

* * * * * *

AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC
TTT GGG TTC CTG TGG GAG TAC TAG AGG GCC TGG GGA CTC CAG TGT ACG CAC CAC CAC CTG
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp>

850 860 870 880 890 900

* * * * * *

GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT
CAC TCG GTG CTT CTG GGA CTC CAG TTC AAG TTG ACC ATG CAC CTG CCG CAC CTC CAC GTC
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His>

910 920 930 940 950 960

* * * * * *

AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC GTC
TTA CGG TTC TGT TTC GGC GCC CTC CTC GTC ATG TTG TCG TGC ATG GCA CAC CAG TCG CAG
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val>

970 980 990 1000 1010 1020

* * * * * *

CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC
GAG TGG CAG GAC GTG GTC CTG ACC GAC TTA CCG TTC CTC ATG TTC ACG TTC CAG AGG TTG
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn>

1030 1040 1050 1060 1070 1080

* * * * * *

AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA
TTT CGG GAG GGT CGG GGG TAG CTC TTT TGG TAG AGG TTT CGG TTT CCC GTC GGG GCT CTT
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu>



Fig.15C.

1090	1100	1110	1120	1130	1140
*	*	*	*	*	*
CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG	GGT GTC CAC ATG TGG GAC GGG GGT AGG GCC CTA CTC GAC TGG TTC TTG GTC CAG TCG GAC	Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu>			
1150	1160	1170	1180	1190	1200
*	*	*	*	*	*
ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG	TGG ACG GAC CAG TTT CCG AAG ATA GGG TCG CTG TAG CGG CAC CTC ACC CTC TCG TTA CCC	Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly>			
1210	1220	1230	1240	1250	1260
*	*	*	*	*	*
CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC	GTC GGC CTC TTG TTG ATG TTC TGG TGC GGA GGG CAC GAC CTG AGG CTG CCG AGG AAG AAG	Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe>			
1270	1280	1290	1300	1310	1320
*	*	*	*	*	*
CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC	GAG ATG TCG TTC GAG TGG CAC CTG TTC TCG TCC ACC GTC GTC CCC TTG CAG AAG AGT ACG	Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys>			
1330	1340	1350	1360	1370	1380
*	*	*	*	*	*
TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG	AGG CAC TAC GTA CTC CGA GAC GTG TTG GTG ATG TGC GTC TTC TCG GAG AGG GAC AGA GGC	Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro>			
* GGT AAA TGA CCA TTT ACT Gly Lys ****>					



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Fig.16A.

10	20	30	40	50	60
*	*	*	*	*	*
ATG GTC AGC TAC TGG GAC ACC GGG GTC CTG CTG TGC GCG CTG CTC AGC TGT CTG CTT CTC TAC CAG TCG ATG ACC CTG TGG CCC CAG GAC ACG CGC GAC GAG TCG ACA GAC GAA GAG Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser Cys Leu Leu Leu>					
70	80	90	100	110	120
*	*	*	*	*	*
ACA GGA TCT AGT TCA GGT TCA AAA TTA AAA GAT CCT GAA CTG AGT TTA AAA GGC ACC CAG TGT CCT AGA TCA AGT CCA AGT TTT AAT TTT CTA GGA CTT GAC TCA AAT TTT CCG TGG GTC Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro Glu Leu Ser Leu Lys Gly Thr Gln>					
130	140	150	160	170	180
*	*	*	*	*	*
CAC ATC ATG CAA GCA GGC CAG ACA CTG CAT CTC CAA TGC AGG GGG GAA GCA GCC CAT AAA GTG TAG TAC GTT CGT CCG GTC TGT GAC GTC GAG GTT ACG TCC CCC CTT CGT CGG GTC TTT His Ile Met Gln Ala Gly Gln Thr Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys>					
190	200	210	220	230	240
*	*	*	*	*	*
TGG TCT TTG CCT GAA ATG GTG AGT AAG GAA AGC GAA AGG CTG AGC ATA ACT AAA TCT GCC ACC AGA AAC GGA CTT TAC CAC TCA TTC CTT TCG CTT TCC GAC TCG TAT TGA TTT AGA CGG Trp Ser Leu Pro Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala>					
250	260	270	280	290	300
*	*	*	*	*	*
TGT GGA AGA AAT GGC AAA CAA TTC TGC AGT ACT TTA ACC TTG AAC ACA GCT CAA GCA AAC ACA CCT TCT TTA CCG TTT GTT AAG ACG TCA TGA AAT TGG AAC TTG TGT CGA GTT CGT TTG Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr Ala Gln Ala Asn>					
310	320	330	340	350	360
*	*	*	*	*	*
CAC ACT GGC TTC TAC AGC TGC AAA TAT CTA GCT GTA CCT ACT TCA AAG AAG AAG GAA ACA GTG TGA CCG AAG ATG TCG ACG TTT ATA GAT CGA CAT GGA TGA AGT TTC TTC CTT TGT His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val Pro Thr Ser Lys Lys Glu Thr>					
370	380	390	400	410	420
*	*	*	*	*	*
GAA TCT GCA ATC TAT ATA TTT ATT AGT GAT ACA GGT AGA CCT TTC GTA GAG ATG TAC AGT CTT AGA CGT TAG ATA TAT AAA TAA TCA CTA TGT CCA TCT GGA AAG CAT CTC TAC ATG TCA Glu Ser Ala Ile Tyr Ile Phe Ile Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser>					
430	440	450	460	470	480
*	*	*	*	*	*
GAA ATC CCC GAA ATT ATA CAC ATG ACT GAA GGA AGG GAG CTC GTC ATT CCC TGC CGG GTT CTT TAG GGG CTT TAA TAT GTG TAC TGA CTT CCT TCC CTC GAG CAG TAA GGG ACG GCC CAA Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val>					
490	500	510	520	530	540
*	*	*	*	*	*
ACG TCA CCT AAC ATC ACT GTT ACT TTA AAA AAG TTT CCA CTT GAC ACT TTG ATC CCT GAT TGC AGT GGA TTG TAG TGA CAA TGA AAT TTT TTC AAA GGT GAA CTG TGA AAC TAG GGA CTA Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp>					



Fig. 16B.



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Fig.16C.

1090 1100 1110 1120 1130 1140
 * * * * * * * * * * * * *
 TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA
 AAG GAG AAG GGG GGT TTT GGG TTC CTG TGG GAG TAC TAG AGG GCC TGG GGA CTC CAG TGT
 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr>

 1150 1160 1170 1180 1190 1200
 * * * * * * * * * * * * *
 TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC
 ACG CAC CAC CAC CTG CAC TCG GTG CTT CTG GGA CTC CAG TTC AAG TTG ACC ATG CAC CTG
 Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp>

 1210 1220 1230 1240 1250 1260
 * * * * * * * * * * * * *
 GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG CAG TAC AAC AGC ACG TAC
 CCG CAC CTC CAC GTC TTA CGG TTC TGT TTC GGC GCC CTC CTC GTC ATG TTG TCG TGC ATG
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr>

 1270 1280 1290 1300 1310 1320
 * * * * * * * * * * * * *
 CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG
 GCA CAC CAG TCG CAG GAG TGG CAG GAC GTG GTC CTG ACC GAC TTA CGG TTC CTC ATG TTC
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys>

 1330 1340 1350 1360 1370 1380
 * * * * * * * * * * * * *
 TGC AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA
 ACG TTC CAG AGG TTG TTT CGG GAG GGT CGG GGG TAG CTC TTT TGG TAG AGG TTT CGG TTT
 Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys>

 1390 1400 1410 1420 1430 1440
 * * * * * * * * * * * * *
 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG
 CCC GTC GGG GCT CTT GGT GTC CAC ATG TGG GAC GGG GGT AGG GCC CTA CTC GAC TGG TTC
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys>

 1450 1460 1470 1480 1490 1500
 * * * * * * * * * * * * *
 AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG
 TTG GTC CAG TCG GAC TGG ACG GAC CAG TTT CCG AAG ATA GGG TCG CTG TAG CGG CAC CTC
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu>

 1510 1520 1530 1540 1550 1560
 * * * * * * * * * * * * *
 TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC
 ACC CTC TCG TTA CCC GTC GGC CTC TTG TTG ATG TTC TGG TGC GGA GGG CAC GAC CTG AGG
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser>

 1570 1580 1590 1600 1610 1620
 * * * * * * * * * * * * *
 GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG
 CTG CGG AGG AAG AAG GAG ATG TCG TTC GAG TGG CAC CTG TTC TCG TCC ACC GTC GTC CCC
 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly>



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Fig. 16D.

1630 1640 1650 1660 1670 1680

1640

1650

1660

1670

1680

AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC
 TTG CAG AAG AGT ACG AGG CAC TAC GTA CTC CGA GAC GTG TTG GTG ATG TGC GTC TTC TCG
 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser>

1690

1700

```

*   *   *   *
TCC CTG TCT CCG GGT AAA TGA
AGG GAC AGA GGC CCA TTT ACT
Ser Leu Ser Pro Gly Lys ***>

```

卷之三



Fig.17.

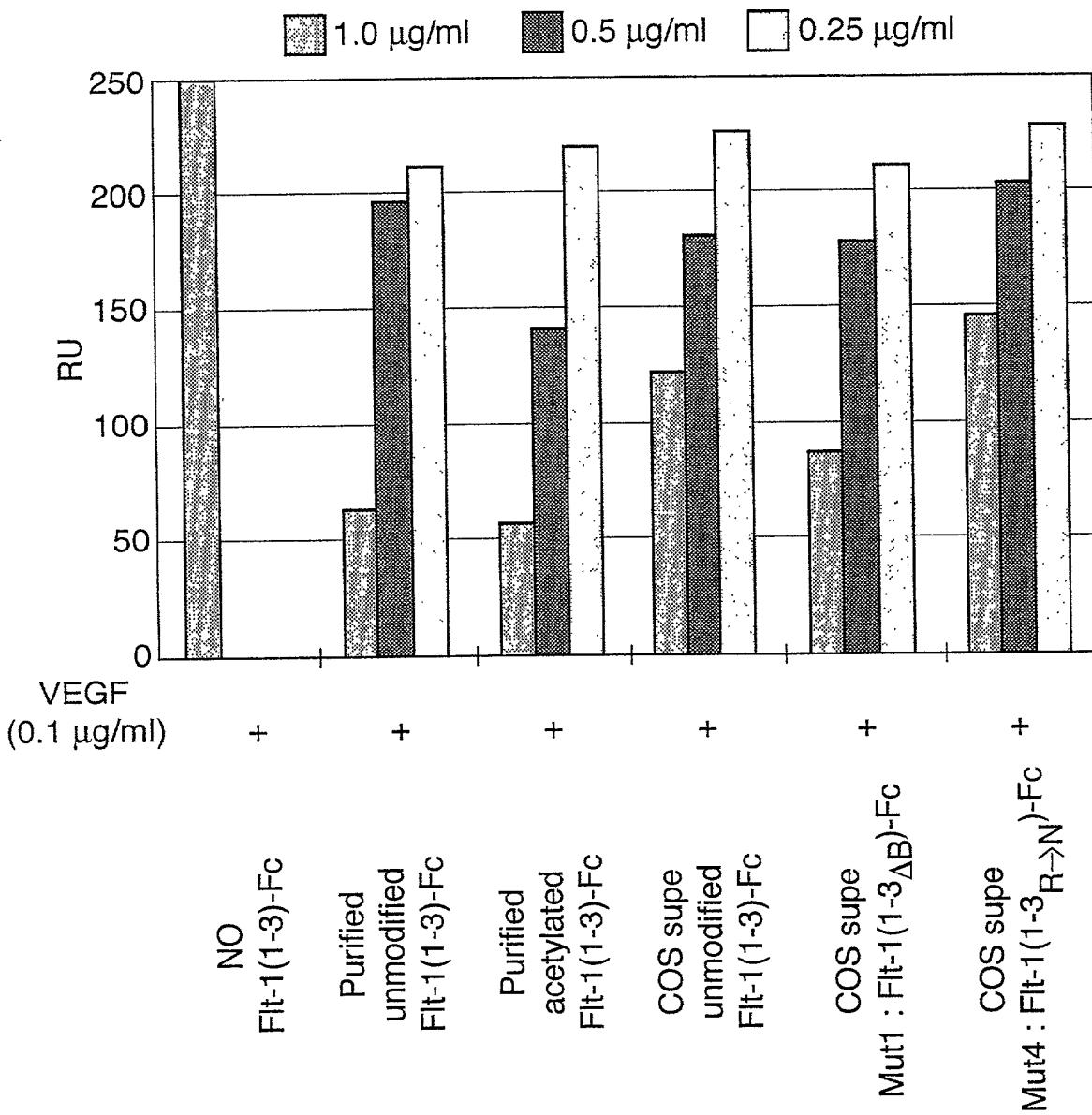




Fig.18.

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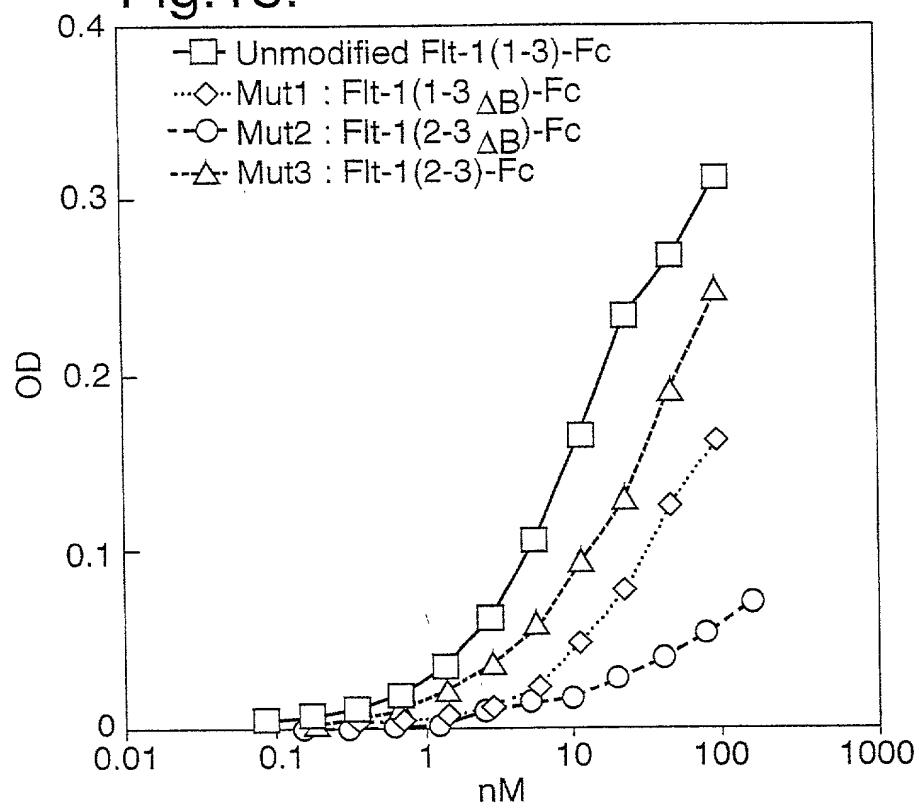


Fig.19.

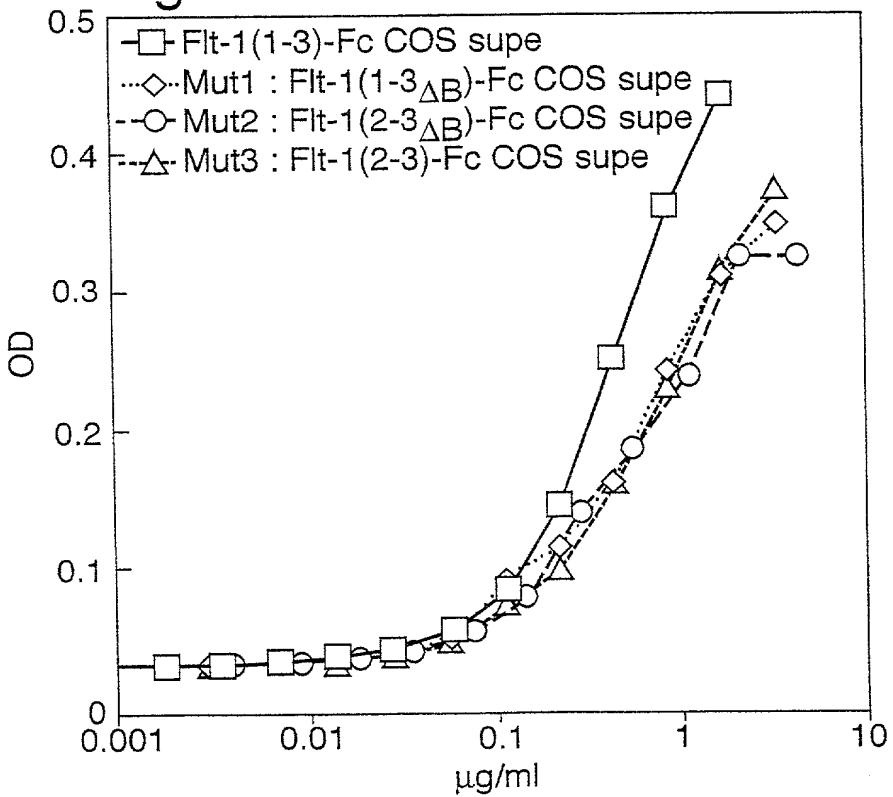
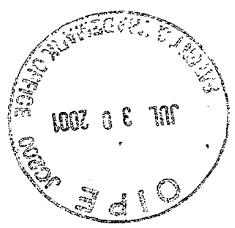
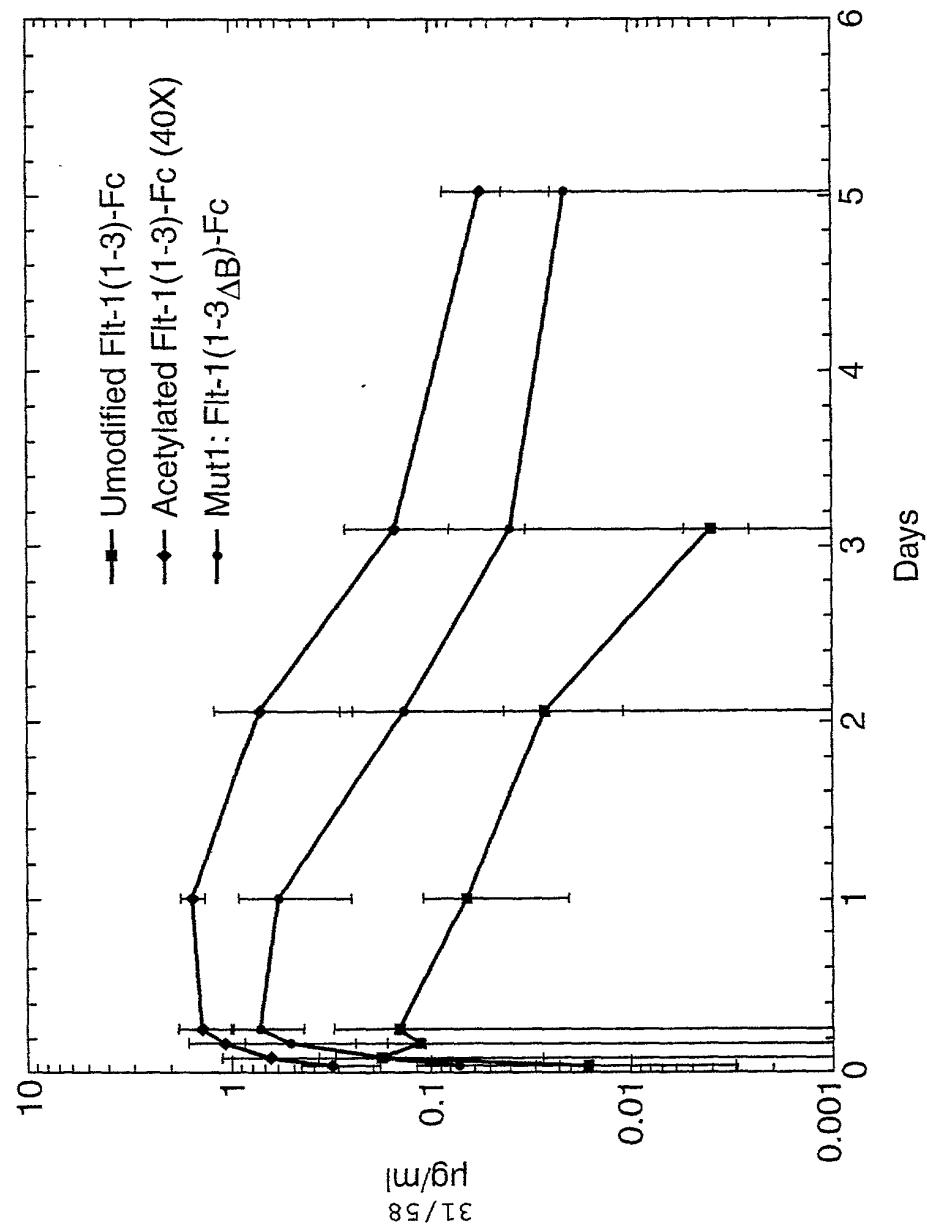


Fig.20.





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Fig.21A.

>EcoRI_site
 10 20 30 40 50 60 70 80
 AAGCTTGGGCTCCAGGTCGATCGACTCTAGAGGATCGATCCCCGGCGAGCTCGAATTGCGAACCAACCATTGGTCAGCTAC
 TTGCAACCCGACGTCCAGCTAGCTGAGATCTCCTAGCTAGGGGCCGCTCGAGCTTAAGCGTTGGTGGTACCAAGTCGATG
 M V S Y>
 1 4
 >

 >BspEI_bridge
 90 100 110 120 130 140 150 160
 TGGGACACCGGGGTCCCTGCTGTGCGCGCTGCTCACGCTGCTGCTTCACAGGATCTAGTTCCGGAGGTAGACCTTCGCT
 ACCCTGTTGCCCCAGGACGACACGCGCACGAGTCGACAGACGAAGAGTGTCTAGATCAAGGCCCTCCATCTGGAAAGCA
 W D T G V L L C A L L S C L L L T G S S>
 FLT1 SS
 >
 S G>
 >
 G R P F V>
 31
 >

 170 180 190 200 210 220 230 240
 AGAGATGTACAGTGAATCCCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGTTACGTCAC
 TCTCTACATGTCACTTTAGGGCTTATATGTGTACTGACTTCCTCCCTCGAGCAGTAAGGGACGGCCAATGCACTG
 E M Y S E I P E I I H M T E G R E L V I P C R V T S>
 57
 >
 HFLT1 D2
 >

 250 260 270 280 290 300 310 320
 CTAACATCACTGTTACTTTAAAAAGTTCCACTTGACACTTTGATCCCTGATGGAAAACGATAATCTGGGACAGTAGA
 GATGTTAGTGACAATGAAATTCTCAAGGTGAACTGTTAGGGACTACCTTTGCGTATTAGACCCCTGTCATCT
 P N I T V T L K K F P L D T L I P D G K R I I W D S R>
 84
 >
 HFLT1 D2
 >

 330 340 350 360 370 380 390 400
 AAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATAGGGCTCTGACCTGTGAAGCAACAGTCATGGCATTGTA
 TTCCCGAAGTAGTATAGTTACGTTGCACTGTTATCCCGAAGACTGGACACTTCGTTGTCAGTACCCGTAACAT
 K G F I I S N A T Y K E I G L L T C E A T V N G H L Y>
 111
 >
 HFLT1 D2
 >

 410 420 430 440 450 460 470 480
 TAAGACAAAATCTCACACATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCTCTCATGAAATTGAACTAT
 ATTCTGTTGATAGAGTGTAGCTGTTGGTTATGTTAGTATCTACACCAAGACTCAGGCAGAGTACCTTAACCTGATA
 K T N Y L T H R Q T N T I I D>
 >
 HFLT1 D2
 >
 V V L S P S H G I E L>
 137
 >
 HFLK1 D3
 >



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Fig.21B.

490 500 510 520 530 540 550 560
 CTGGTGGAGAAAAGCTGTCTAAATTGTACAGCAAGAACTGAACATAATGTGGGATTGACTTCAACTGGGAATACCT
 GACAACCTCTTCAACAGAATTAAACATGTCGTCTTGACTTGAATTACACCCCTAACIGAAGTTGACCCATTATGGGA
 S V G E K L V L N C T A R T E L N V G I D F N W E Y P>
 164
 HFLK1 D3_>

570 580 590 600 610 620 630 640
 TCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGACCTAAAAACCCACTCTGGGAGTGAGATGAAGAAATTGGAG
 AGAACGCTTCGTAGTCGTATTCTTGAACATTGGCTCTGGATTGGGTCAAGACCCCTCACTCTACTTCTTTAAAAACTC
 S S K H Q H K K L V N R D L K T Q S G S E M K K F L S>
 191
 HFLK1 D3_>

650 660 670 680 690 700 710 720
 CACCTTAACTATAGATGGTGTAAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGTGATGACCAAGA
 GTGGAATTGATATCTACCACATTGGGCCTCACTGGTCTTAACATGTGGACACGTCGTAGGTCAACCGACTACTGGTCT
 T L T I D G V T R S D Q G L Y T C A A S S G L M T K>
 217
 HFLK1 D3_>

>Srf_Bridge_>
 730 740 750 760 770 780 790 800
 AGAACAGCACATTGTCAGGGTCCATGAAAAGGGCCGGCGACAAAACCTCACACATGCCAACCGTGCCACCTGAA
 TCTTCGTGTAAACAGTCCCAGGTACTTTCCCGGGCCGCTGTTGAGTGTGTACGGTGGCACGGGTGACTGGACTT
 K N S T F V R V H E K>
 HFLK1 D3_>
 G P G>
 D K T H T C P P C P A P E>
 244
 FCAC1 (A)_>

810 820 830 840 850 860 870 880
 CTCCTGGGGGACCGTCAGTCCTCCCTTCCCCAAAACCAAGGACACCCATGATCTCCGGACCCCTGAGGTCAC
 GAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGTTGGGTCTGTGGAGTACTAGAGGGCCTGGGACTCCAGTG
 L L G G P S V F L F P P K P K D T L M I S R T P E V T>
 271
 FCAC1 (A)_>

890 900 910 920 930 940 950 960
 ATGCGTGGTGGTGGACGTGAGCCACGAAGACCCGTAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCAATAATG
 TACGCACCAACACCTGCACTCGTGCTCTGGACTCCAGTTCAAGTTGACCATGCACCTGCCACCTCCACGTATTAC
 C V V V D V S H E D P E V K F N W Y V D G V E V H N>
 297
 FCAC1 (A)_>

970 980 990 1000 1010 1020 1030 1040
 CCAAGACAAAGCCGCGGGAGGAGGCACTACAACACAGCACGTACCGTGTGGTCAGCGTCCCTCACCGTCTGCACCCAGGACTGG
 GGTCTGTGTTGGCGCCCTCTCGTCATGTGTGCGATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACC
 A K T K P R E E Q Y N S T Y R V V S V L T V L H Q D W>
 324
 FCAC1 (A)_>



Fig.21C.

1050 1060 1070 1080 1090 1100 1110 1120
 CTGAATGGCAAGGAGTACAAGTGCAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCAAAGCCAA
 GACTTACCGTTCTCATGTCACGGTCCAGAGGTTGGGGTAGCTCTTGGTAGAGGTTCCGGTT
 L N G K E Y K C K V S N K A L P A P I E K T I S K A K >
 351
 FCAC1 (A) >

>A>C_A_allotype
 |
 >G>T_A_allotype
 |
 1130 1140 1150 1160 1170 1180 1190 1200
 AGGGCAGCCCCGAGAACCAACAGGTGTACACCCCTGCCCATCCCCGGGATGAGCTGACCAAGAACCAACAGGTTCAGCCTGACCT
 TCCCGTGGGGCTCTGGTGTCCACATGTGGACGGGGTAGGGCCCTACTCGACTGGTCTTGGTCCAGTCGGACTGG
 G Q P R E P Q V Y T L P P S R D E L T K N Q V S L T >
 377
 FCAC1 (A) >

1210 1220 1230 1240 1250 1260 1270 1280
 GCCTGGTCAAAGGCTCTATCCCAGCGACATGCCGTGGAGTGGGAGAGCAATGGGAGCCGGAGAACAACTACAAGACC
 CGGACCACTTCCGAAGATAGGTGCGCTGTAGCGGACCCCTCACCCCTCTCGTTACCCGTGGCCTTGTGATGTTCTGG
 C L V K G F Y P S D I A V E W E S N G Q P E N N Y K T >
 404
 FCAC1 (A) >

>T>C
 |
 1290 1300 1310 1320 1330 1340 1350 1360
 ACGCCTCCCGTGGACTCCGACGGCTCTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG
 TGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAGAGATATCGTTGAGTGGCACCTGTTCTCGTCCACCGTCGTCCC
 T P P V L D S D G S F F L Y S K L T V D K S R W Q Q G >
 431
 FCAC1 (A) >

1370 1380 1390 1400 1410 1420 1430 1440
 GAACGTCTCTCATGCTCCGTATGCATGAGGCTCTGCACAAACCAACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGTA
 CTTCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTCTCGGAGAGGGACAGAGGCCAT
 N V F S C S V M H E A L H N H Y T Q K S L S L S P G >
 457
 FCAC1 (A) >

>NotI_site
 |
 | 1450
 AATGAGCGGGCCG
 TTACTCGCCGGCG
 K * >
 458
 >



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Fig.22A.

>EcoRI_site

10	20	30	40	50	60	70	80
AAGCTTGGGCTGCAGGTCGATCGACTCTAGAGGATCGATCCCCGGCGAGCTCGAATTGCGAACCAACCATGGTCAGCTAC							
TTCGAACCCGACGTCCAGCTAGCTGAGATCTCCTAGCTAGGGGCCGCTCGAGCTTAAGCGTTGGTGGTACCAAGTCGATG							
M V S Y>							
1 4							
>							

>BspEI_bridge

90	100	110	120	130	140	150	160
TGGGACACCGGGGCCTGCTGCGCGCTGCTCAGCTGCTGCTCACAGGATCTAGTCCGGAGGTAGACCTTCGT							
ACCCCTGTGGCCCCAGGACGACACGCGCGACAGACAGAAGAGTGTCTAGATCAAGGCCTCCATCTGGAAAGCA							
W D T G V L L C A L L S C L L L T G S S>							
FLT1 SIGNAL SEQUENCE >							
S G>							
>							
G R P F V>							
31							
>							

170 180 190 200 210 220 230 240

AGAGATGTACAGTGAATCCCCGAAATIATACACATGACTGAAGGAAGGGAGCTCGTCATTCCTGCCGGTTACGTAC							
TCTCTACATGTCACTTTAGGGCTTAAATATGTGTACTGACTTCCTCCCTCGAGCAGTAAGGGACGGCCCAATGCACTG							
E M Y S E I P E I I H M T E G R E L V I P C R V T S>							
57							
FLT1 IG DOMAIN 2 >							

250 260 270 280 290 300 310 320

CTAACATCACTGTTACTTTAAAAAGTTTCCACTTGACACTTGATCCCTGATGGAAAACGCATAATCTGGGACAGTAGA							
GATTGTAGTGACAATGAAATTTCAAAGGTGAACGTGAAACTAGGGACTACCTTTGCGTATTAGACCCCTGTCATCT							
P N I T V T L K K F P L D T L I P D G K R I I W D S R>							
84							
FLT1 IG DOMAIN 2 >							

330 340 350 360 370 380 390 400

AAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATAGGGCTCTGACCTGTGAAGCAACAGTCATGGCATTGTA							
TTCCCGAAGTAGTATAGTTACGTTGCACTGTTCTATCCCGAAGACTGGACACTTCGTTGTCAGTACCCGTAAACAT							
K G F I I S N A T Y K E I G L L T C E A T V N G H L Y>							
111							
FLT1 IG DOMAIN 2 >							

410 420 430 440 450 460 470 480

TAAGACAAACTATCTCACACATCGACAAACCAATACAATCATAGATATCCAGCTGTTGCCAGGAAGTCGCTGGAGCTGC							
ATTCTGTTGATAGAGTGTGTAGCTGTTGGTTATGTTAGTATCTATAGGTGACAAACGGGTCCTTCAGCGACCTCGACG							
K T N Y L T H R Q T N T I I D>							
FLT1 IG DOMAIN 2 >							
I Q L L P R K S L E L>							
137							
VEGFR3 (FLT4) IG DOMAIN 3 >							



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Fig.22B.

490 500 510 520 530 540 550 560
 TGGTAGGGAGAAGCTGGTCCTCAACTGCACCGTGTGGGCTGAGTTAACTCAGGTGTCACCTTGACTGGGACTACCCA
 ACCATCCCCTCTCGACCAGGAGTTGACGTGGCACACCCGACTCAAATTGAGTCCACAGTGGAAACTGACCCCTGATGGGT
 L V G E K L V L N C T V W A E F N S G V T F D W D Y P>
 164
 VEGFR3 (FLT4) IG DOMAIN 3 >

570 580 590 600 610 620 630 640
 GGGAAAGCAGGCAGAGCGGGGTAAGTGGTGCCTGAGCGACGCTCCAACAGACCCACACAGAAACTCTCCAGCATCCTGAC
 CCCTTCGTCGCTCGCCCCATTACCCACGGGCTCGCTGCGAGGGTTGCTGGGTGTCCTGAGAGGTGCTAGGACTG
 G K Q A E R G K W V P E R R S Q Q T H T E L S S I L T>
 191
 VEGFR3 (FLT4) IG DOMAIN 3 >

650 660 670 680 690 700 710 720
 CATCCACAAACGTCAGCCAGCACGACCTGGGCTCGTATGTGCAAGGCCAACACGGCATCCAGCGATTGGAGAGCA
 GTAGGTGTTGCAGTCGGTCGCTGGACCCGAGCATAACACACGTCCGGTTGTTGCCGTAGGTGCTAAAGCCCTCTCGT
 I H N V S Q H D L G S Y V C K A N N G I Q R F R E S>
 217
 VEGFR3 (FLT4) IG DOMAIN 3 >

730 740 750 760 770 780 790 800
 CCGAGGTCATTGTCATGAAAATGGCCGGGGGAGACAAAACCTCACACATGCCAACCGTGCCCAAGGCACCTGAACTCTGGGG
 GGCTCCAGTAACACGTAACCTTACCGGGCCCGTGTGAGTGTACGGGTGGCACGGCTGGACTTGAGGACCC
 T E V I V H E N>
 VEGFR3 (FLT4) IG >
 G P G>
 D K T H T C P P C P A P E L L G>
 244
 FCAC1 - A ALLOTYPE >

810 820 830 840 850 860 870 880
 GGACCGTCAGTCCTCCTCTTCCCCCAAAACCCAAGGGACACCCCTCATGATCTCCGGACCCCTGAGGTGACATGCGTGGT
 CCTGGCAGTCAGAAGGGAGAAGGGGGTTGGGTTCTGTGGACTACTAGAGGGCTGGGACTCCAGTGTACGCACCA
 G P S V F L F P P K P K D T L M I S R T P E V T C V V>
 271
 FCAC1 - A ALLOTYPE >

890 900 910 920 930 940 950 960
 GGTGGACGTGAGGCCACGAAGACCCCTGAGGTCAAGTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAA
 CCACCTGCACCTGGTGCTCTGGACTCCAGTTCAAGTGTACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTT
 V D V S H E D P E V K F N W Y V D G V E V H N A K T>
 297
 FCAC1 - A ALLOTYPE >

970 980 990 1000 1010 1020 1030 1040
 AGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCTGCACCCAGGACTGGCTGAATGGC
 TCGGGCGCCCTCTCGTCATGTTGTCGTCATGGCACACCAGTCGCAAGGAGTGGCAGGACGTGGTCTGACCGACTTACCG
 K P R E E Q Y N S T Y R V V S V L T V L H Q D W L N G>
 324
 FCAC1 - A ALLOTYPE >



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Fig.22C.

1050 1060 1070 1080 1090 1100 1110 1120
 AAGGAGTACAAGTGCAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCC
 TTCCCTCATGTTCACGTTCCAGAGGTTGGTGGGGAGGGTAGCTCTTTGGTAGAGGTTTCGGTTTCCCGTCGG
 K E Y K C K V S N K A L P A P I E K T I S K A K G Q P>
 351

FCΔC1 - A ALLOTYPE

>A>C_A_allotype

>G>T_A_allotype

1130 1140 1150 1160 1170 1180 1190 1200
 CCGAGAACACAGGTGTACACCCCTGCCCTGCCCTGGATGAGCTGACCAAGAACCCAGGTCAAGCTGACCTGCCTGGTCA
 GGCTCTTGGTGTCCACATGTGGACGGGGTAGGGCCCTACTCGACTGGTCTTGGTCCAGTCGGACTGGACGGACCAGT
 R E P Q V Y T L P P S R D E L T K N Q V S L T C L V>
 377

FCΔC1 - A ALLOTYPE

1210 1220 1230 1240 1250 1260 1270 1280
 AAGGCTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGCAGCCGGAGAACAACTACAAGACCACGCCCTCCC
 TTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCCTCGTTACCCGTCGGCCCTTGTIGATGTTCTGGTGCAGGGAGGG
 K G F Y P S D I A V E W E S N G Q P E N N Y K T T P P>
 404

FCΔC1 - A ALLOTYPE

>T>C

1290 1300 1310 1320 1330 1340 1350 1360
 GTGCTGGACTCCGACGGCTCCTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGAACGTCTT
 CACGACCTGAGGCTGCCAGGAAGAAGGAGATATCGTCAGTGGCACCTGTCTCGTCCACCGTGTCCCCCTTGCAGAA
 V L D S D G S F F L Y S K L T V D K S R W Q Q G N V F>
 431

FCΔC1 - A ALLOTYPE

>NotI_site

1370 1380 1390 1400 1410 1420 1430 1440
 CTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAATGACCGG
 GAGTACGAGGCACCTACGTACTCCGAGACGTGTTGGTGTGCGCTCTCGGAGAGGGACAGAGGCCATTACTCGCC
 S C S V M H E A L H N H Y T Q K S L S L S P G K *>
 455

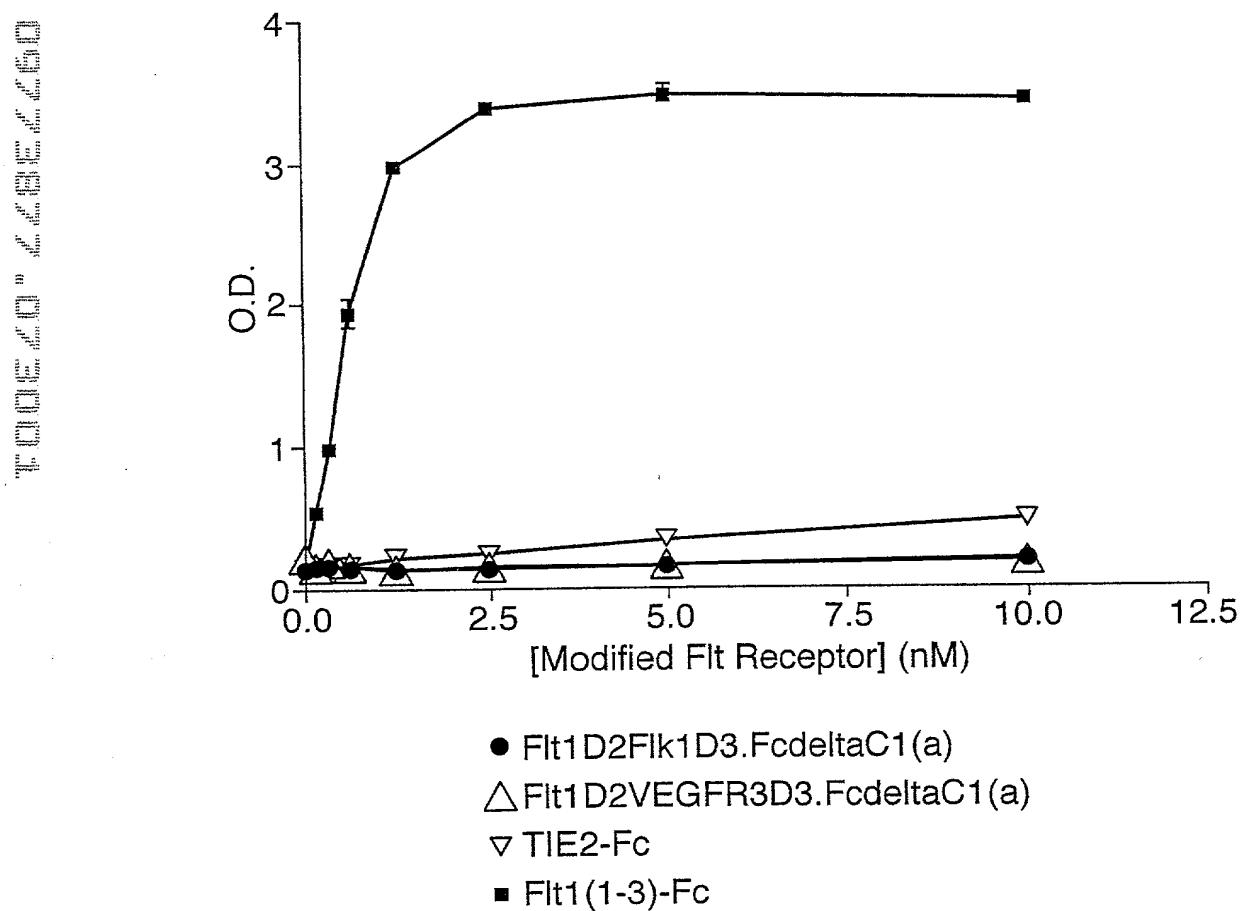
FCΔC1 - A ALLOTYPE

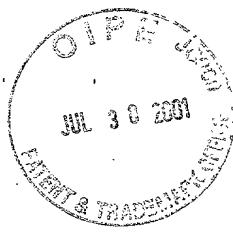
CCGC
GGCG



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Fig.23.





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Fig.24A.

10 20 30 40 50 60
 * * * * * *
 ATG GTC AGC TAC TGG GAC ACC GGG GTC CTG CTG TGC GCG CTG CTC AGC TGT CTG CTT CTC
 TAC CAG TCG ATG ACC CTG TGG CCC CAG GAC GAC CGC GAC GAG TCG ACA GAC GAA GAG
 M V S Y W D T G V L L C A L L S C L L L>
 1 5 hFLT1 SIGNAL SEQUENCE 15 20>

70 80 90 100 110 120
 * * * * * *
 ACA GGA TCT AGT TCC GGA AGT GAT ACC GGT AGA CCT TTC GTC GAG ATG AGT GAA ATC
 TGT CCT AGA TCA AGG CCT TCA CTA TGG CCA TCT GGA AAG CAT CTC TAC ATG TCA CTT TAG
 T G S S S G>
 21 hFLT1 SIGNAL SEQ 26>
 S D T G R P F V E M Y S E I>
 27 30 hFLT1 IG DOMAIN 2 40>

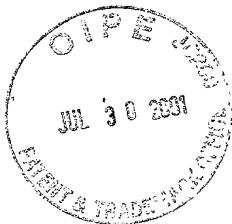
130 140 150 160 170 180
 * * * * * *
 CCC GAA ATT ATA CAC ATG ACT GAA GGA AGG GAG CTC GTC ATT CCC TGC CGG GTT ACG TCA
 GGG CTT TAA TAT GTG TAC TGA CTT CCT CTC GAG CAG TAA GGG ACG GCC CAA TGC AGT
 P E I I H M T E G R E L V I P C R V T S>
 41 45 hFLT1 IG DOMAIN 2 55 60>

190 200 210 220 230 240
 * * * * * *
 CCT AAC ATC ACT GTT ACT TTA AAA AAG TTT CCA CTT GAC ACT TTG ATC CCT GAT GGA AAA
 GGA TTG TAG TGA CAA TGA AAT TTT TTC AAA GGT GAA CTG TGA AAC TAG GGA CTA CCT TTT
 P N I T V T L K K F P L D T L I P D G K>
 61 65 hFLT1 IG DOMAIN 2 75 80>

250 260 270 280 290 300
 * * * * * *
 CGC ATA ATC TGG GAC AGT AGA AAG GGC TTC ATC ATA TCA AAT GCA ACG TAC AAA GAA ATA
 GCG TAT TAG ACC CTG TCA TCT TTC CGG AAG TAG TAT AGT TTA CGT TGC ATG TTT CTT TAT
 R I I W D S R K G F I I S N A T Y K E I>
 81 85 hFLT1 IG DOMAIN 2 95 100>

310 320 330 340 350 360
 * * * * * *
 GGG CTT CTG ACC TGT GAA GCA ACA GTC AAT GGG CAT TTG TAT AAG ACA AAC TAT CTC ACA
 CCC GAA GAC TGG ACA CTT CGT TGT CAG TTA CCC GTC AAC ATA TTC TGT TTG ATA GAG TGT
 G L L T C E A T V N G H L Y K T N Y L T>
 101 105 hFLT1 IG DOMAIN 2 115 120>

370 380 390 400 410 420
 * * * * * *
 CAT CGA CAA ACC AAT ACA ATA GAT GTG GTT CTG AGT CCG TCT CAT GGA ATT GAA CTA
 GTA GCT GTT TGG TTA TGT TAG TAT CTA CAC CAA GAC TCA GGC AGA GTC CCT TAA CTT GAT
 H R Q T N T I I D>
 121 hFLT1 IG DOMAIN 2 129>
 V V L S P S H G I E L>
 130 hFLT1 IG DOMAIN 3 140>



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Fig. 24B.

430 * 440 * 450 * 460 * 470 * 480 *

 TCT GTT GGA GAA AAG CTT GTC TTA AAT TGT ACA GCA AGA ACT GAA CTA AAT GTG GGG ATT

 AGA CAA CCT CTT TTC GAA CAG AAT TTA ACA TGT CGT TCT TGA CTT GAT TTA CAC CCC TAA

 S V G E K L V L N C T A R T E L N V G I>

 141 145 hFLK1 IG DOMAIN 3 155 160>

 490 * 500 * 510 * 520 * 530 * 540 *

 GAC TTC AAC TGG GAA TAC CCT TCT TCG AAG CAT CAG CAT AAG AAA CTT GTA AAC CGA GAC

 CTG AAG TTG ACC CTT ATG GGA AGA AGC TTC GTC GTA TTC TTT GAA CAT TTG GCT CTG

 D F N W E Y P S S K H Q H K K L V N R D>

 161 165 hFLK1 IG DOMAIN 3 175 180>

 550 * 560 * 570 * 580 * 590 * 600 *

 CTA AAA ACC CAG TCT GGG AGT GAG ATG AAG AAA TTT TTG AGC ACC TTA ACT ATA GAT GGT

 GAT TTT TGG GTC AGA CCC TCA CTC TAC TTC TTT AAA AAC TCG TGG AAT TGA TAT CTA CCA

 L K T Q S G S E M K K F L S T L T I D G>

 181 185 hFLK1 IG DOMAIN 3 195 200>

 610 * 620 * 630 * 640 * 650 * 660 *

 GTA ACC CGG AGT GAC CAA GGA TTG TAC ACC TGT GCA GCA TCC AGT GGG CTG ATG ACC AAG

 CAT TGG GCC TCA CTG GTT CCT AAC ATG TGG ACA CGT CGT AGG TCA CCC GAC TAC TGG TTC

 V T R S D Q G L Y T C A A S S G L M T K>

 201 205 hFLK1 IG DOMAIN 3 215 220>

 670 * 680 * 690 * 700 * 710 * 720 *

 AAG AAC AGC ACA TTT GTC AGG GTC CAT GAA AAG GAC AAA ACT CAC ACA TGC CCA CCG TGC

 TTC TTG TCG TGT AAA CAG TCC CAG GTA CTT TTC CTG TTT TGA GTG TGT ACG GGT GGC ACG

 K N S T F V R V H E K>

 221 hFLK1 IG DOMAIN 3 231>

 232 D K T H T C P P C>

 hFCAC1 A 240>

 730 * 740 * 750 * 760 * 770 * 780 *

 CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC CCC CCA AAA CCC AAG GAC

 GGT CGT GGA CCT GAG GAC CCC CCT GGC AGT CAG AAG GAG AAG GGG GGT TTT GGG TTC CTG

 P A P E L L G G P S V F L F P P K P K D>

 241 245 hFCAC1 A 255 260>

 790 * 800 * 810 * 820 * 830 * 840 *

 ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC GAA

 TGG GAG TAC TAG AGG GCC TGG GGA CTC CAG TGT AGC CAC CAC CAC CTG CAC TOG GTG CTT

 T L M I S R T P E V T C V V V D V S H E>

 261 265 hFCAC1 A 275 280>

 850 * 860 * 870 * 880 * 890 * 900 *

 GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA

 CTG GGA CTC CAG TTC AAG TTG ACC ATG CAC CTG CCG CAC CTC CAC GTA TTA CGG TTC TGT

 D P E V K F N W Y V D G V E V H N A K T>

 281 285 hFCAC1 A 295 300>



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Fig.24C.

910	920	930	940	950	960
*	*	*	*	*	*
AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG					
TTC GGC GCC CTC CTC GTC ATG TTG TCG ATG GCA CAC CAG TCG CAG GAG TGG CAG GAC					
K P R E E Q Y N S T Y R V V S V L T V L>					
301	305	hFCAC1 A	315	320>	
970	980	990	1000	1010	1020
*	*	*	*	*	*
CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA					
GTG GTC CTG ACC GAC TTA CCG TTC CTC ATG TTC ACG TTC CAG AGG TTG TTT CGG GAG GGT					
H Q D W L N G K E Y K C K V S N K A L P>					
321	325	hFCAC1 A	335	340>	
1030	1040	1050	1060	1070	1080
*	*	*	*	*	*
GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA CCA CAG GTG TAC					
CGG GGG TAG CTC TTT TGG TAG AGG TTT CGG TTT CCC GTC GGG GCT CTT GGT GTC CAC ATG					
A P I E K T I S K A K G Q P R E P Q V Y>					
341	345	hFCAC1 A	355	360>	
1090	1100	1110	1120	1130	1140
*	*	*	*	*	*
ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC					
TGG GAC GGG GGT AGG GCC CTC CTC GAC TGG TTC TTG GTC CAG TCG GAC TGG ACG GAC CAG					
T L P P S R D E L T K N Q V S L T C L V>					
361	365	hFCAC1 A	375	380>	
1150	1160	1170	1180	1190	1200
*	*	*	*	*	*
AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC					
TTT CCG AAG ATA GGG TCG CTG TAG CGG CAC CTC ACC CTC TCG TTA CCC GTC GGC CTC TTG					
K G F Y P S D I A V E W E S N G Q P E N>					
381	385	hFCAC1 A	395	400>	
1210	1220	1230	1240	1250	1260
*	*	*	*	*	*
AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG					
TTG ATG TTC TGG TGC GGA GGG CAC GAC CTG AGG CGG AGG AAG AAG GAG ATG TCG TTC					
N Y K T T P V L D S D G S F F L Y S K>					
401	405	hFCAC1 A	415	420>	
1270	1280	1290	1300	1310	1320
*	*	*	*	*	*
CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TCC TCA TGC TCC GTG ATG CAT					
GAG TGG CAC CTG TTC TCG TCC ACC GTC GTC CCC TTG CAG AAG AGT ACG AGG CAC TAC GTA					
L T V D K S R W Q Q G N V F S C S V M H>					
421	425	hFCAC1 A	435	440>	
1330	1340	1350	1360	1370	
*	*	*	*	*	
GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA TGA					
CTC CGA GAC GTG TTG GTG ATG TGC GTC TTC TCG GAG AGG GAC AGA GGC CCA TTT ACT					
E A L H N H Y T Q K S L S L S P G K *>					
441	445	hFCAC1 A	455	458	>



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Fig.25A.

DME - Challenge
+ Flt1D2VEGFR3D3.Fc Δ C1(a)
+ Flt1D2Flk1D3.Fc Δ C1(a)
+ R \rightarrow C
+ NAS
+ Δ B2
+ A40
+ Flt1 (1-3) Fc
VEGF 165

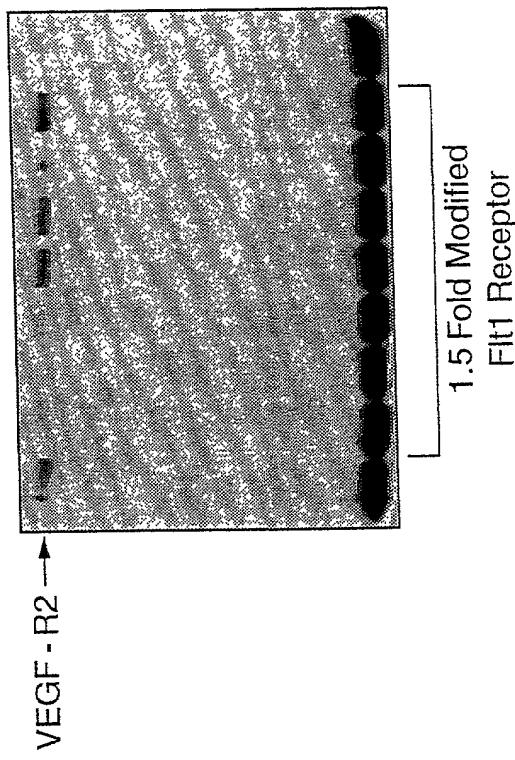
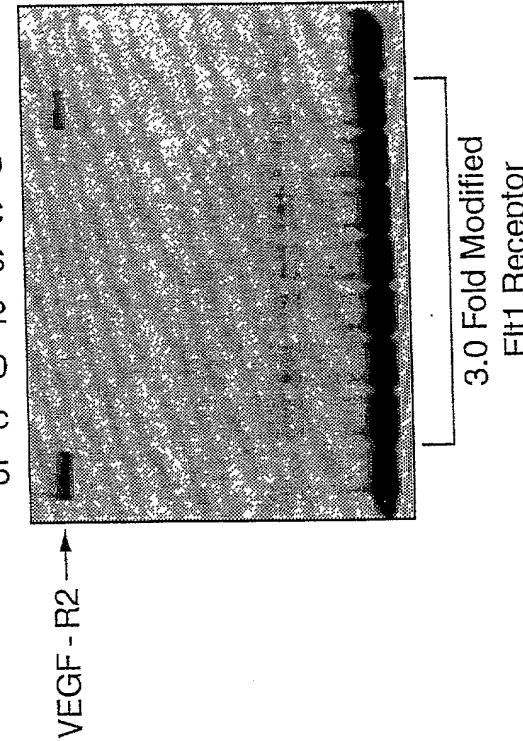


Fig.25B.

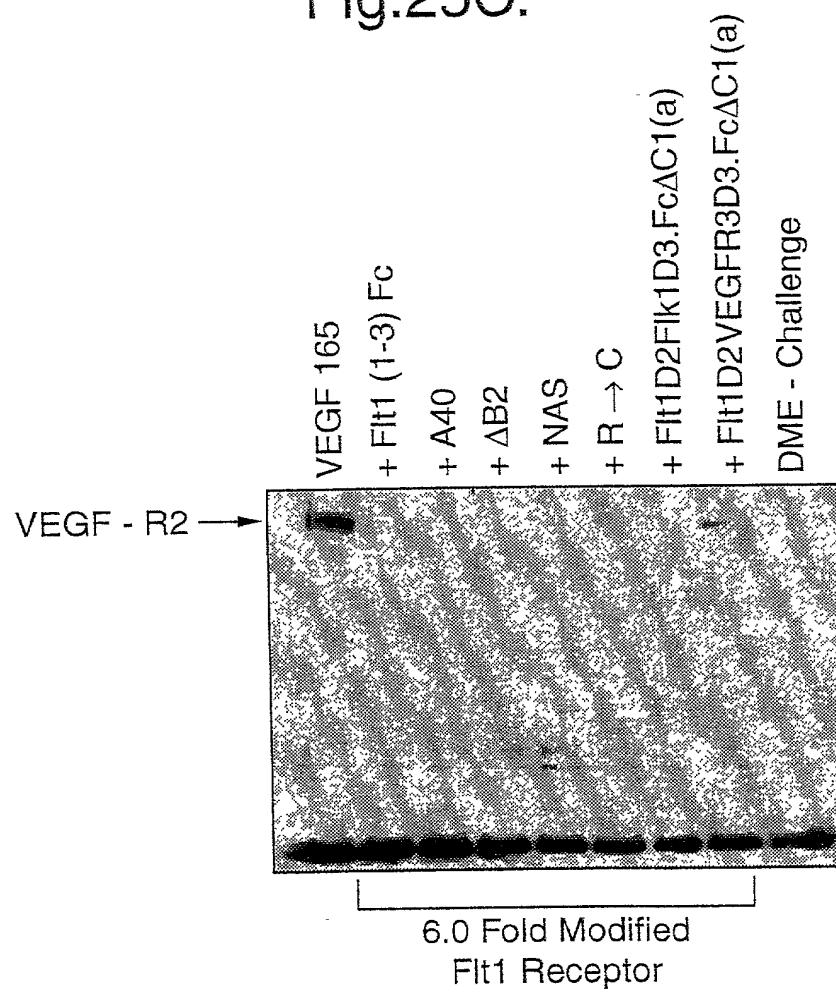
DME - Challenge
+ Flt1D2VEGFR3D3.Fc Δ C1(a)
+ Flt1D2Flk1D3.Fc Δ C1(a)
+ R \rightarrow C
+ NAS
+ Δ B2
+ A40
+ Flt1 (1-3) Fc
VEGF 165





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Fig.25C.



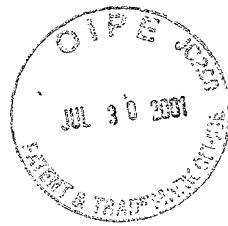


Fig.26A.

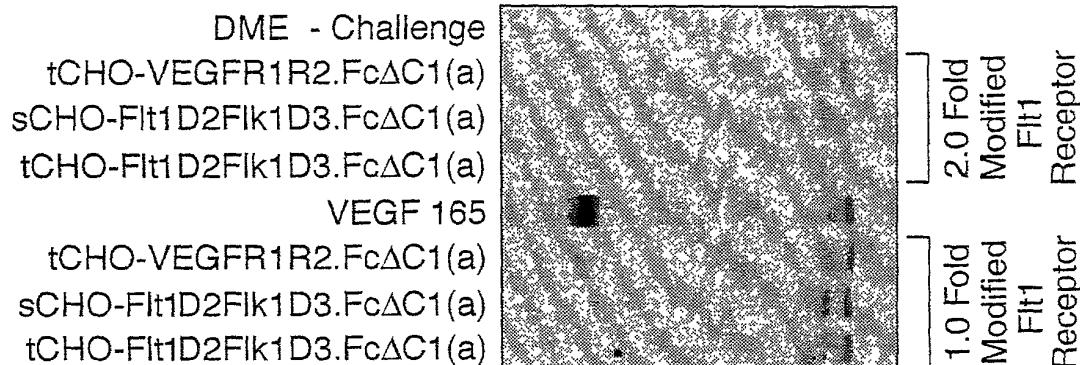


Fig.26B.

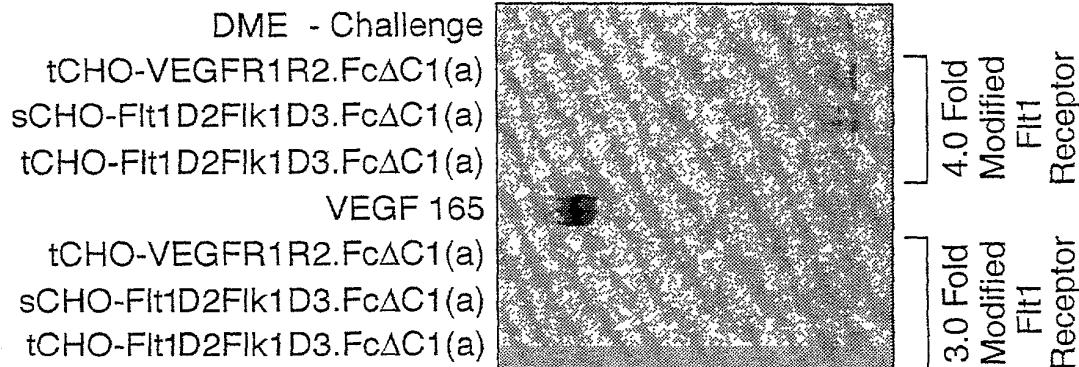


Fig. 27.

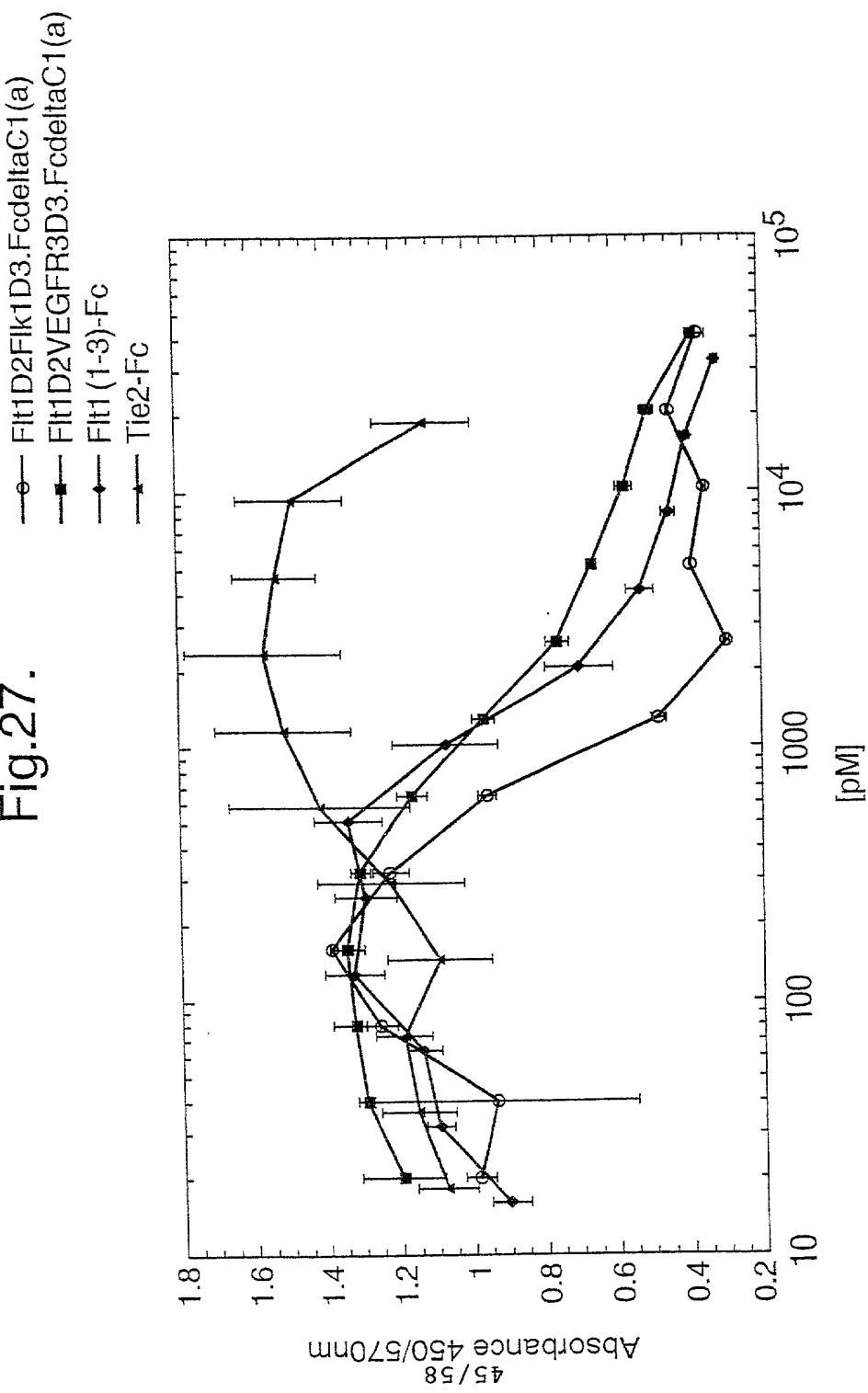
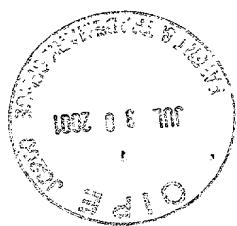


Fig.28.

Binding Stoichiometry of hVEGF165 to Flt1D2Flk1D3.FcΔC1(a) & VEGFR1R2-FcΔC1(a)

hVEGF165 (nM)	VEGF/Flt1D2Flk1D3.FcΔC1(a)	VEGF/VEGFR1R2-FcΔC1(a)
1	0.93	0.98
10	0.97	0.94
50	1	0.99
Average ± StDev	0.96 ± 0.03	0.97 ± 0.02

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Fig.29.

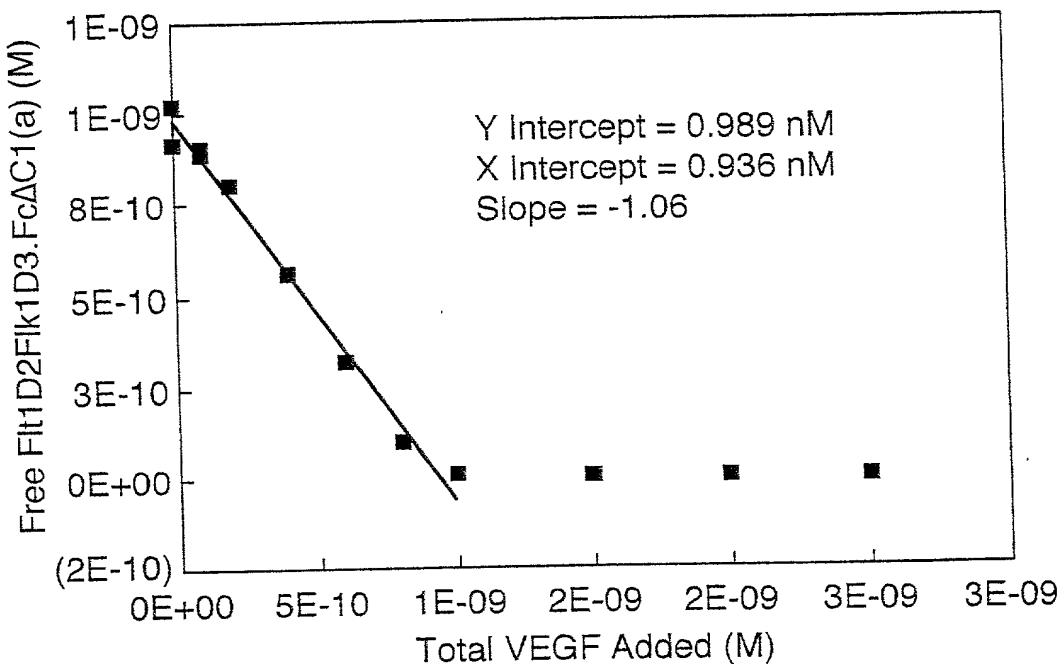
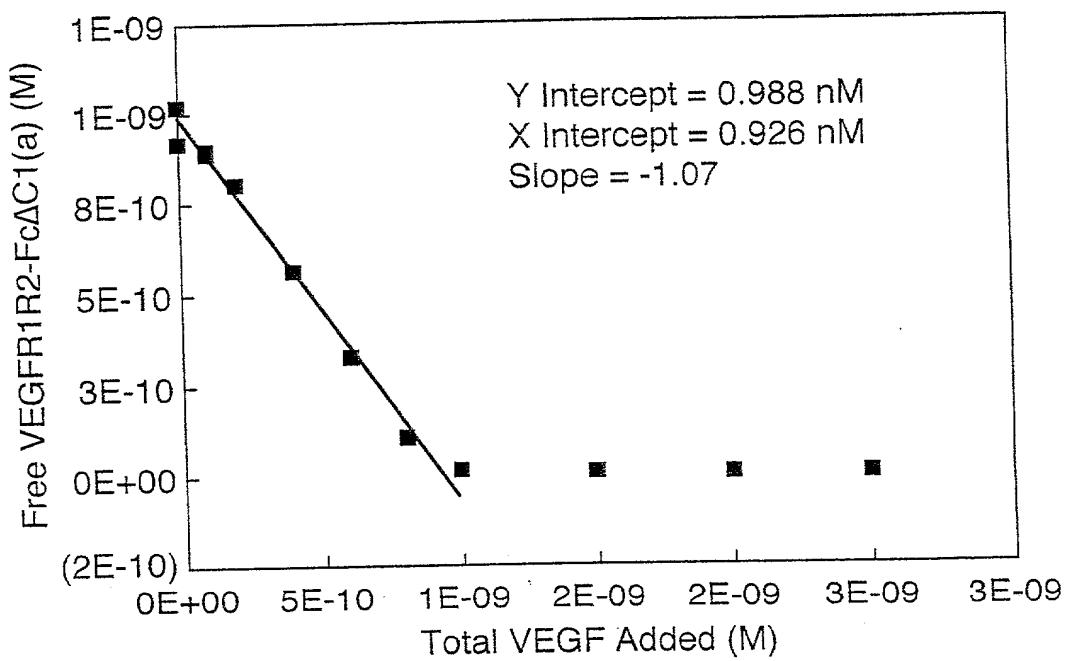
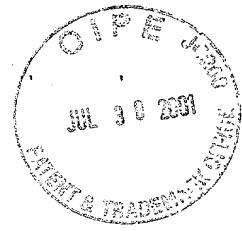


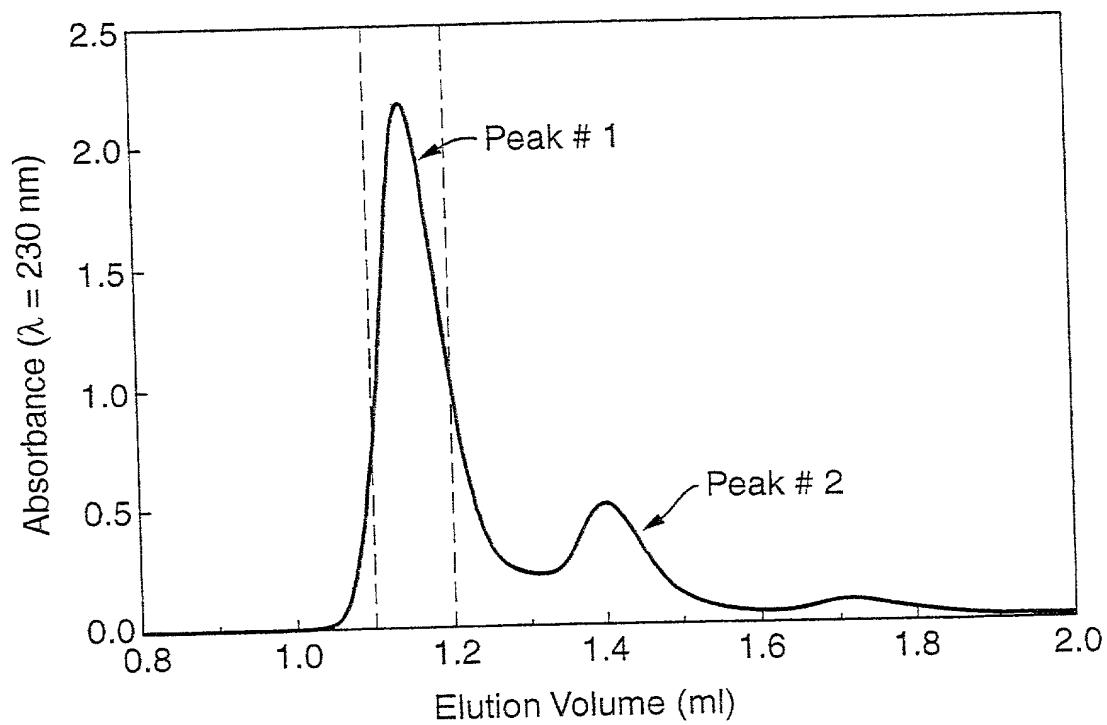
Fig.30.





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Fig.31.





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Fig.32.

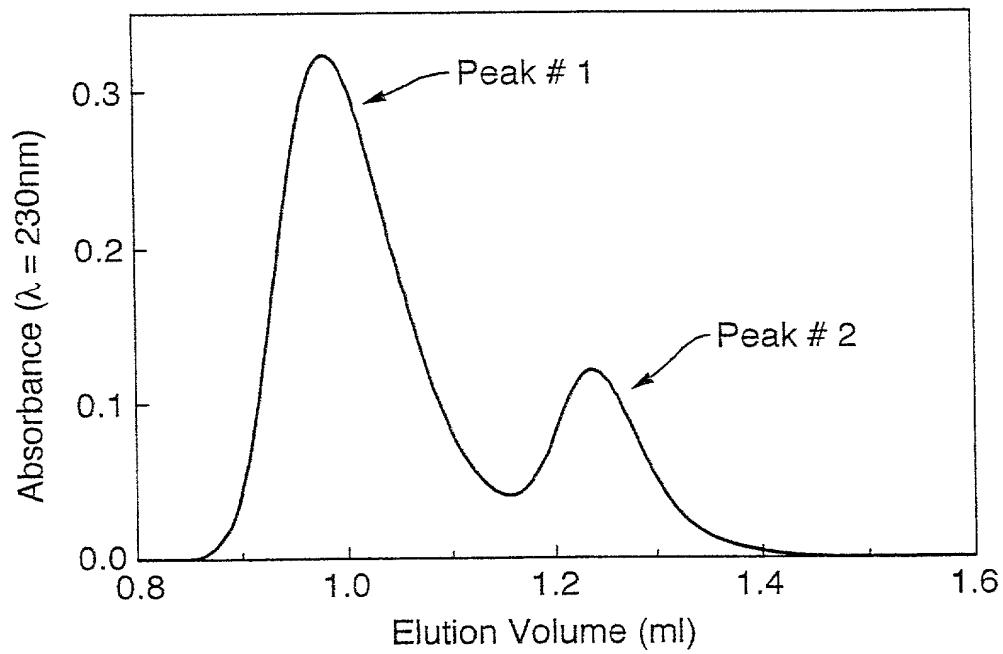
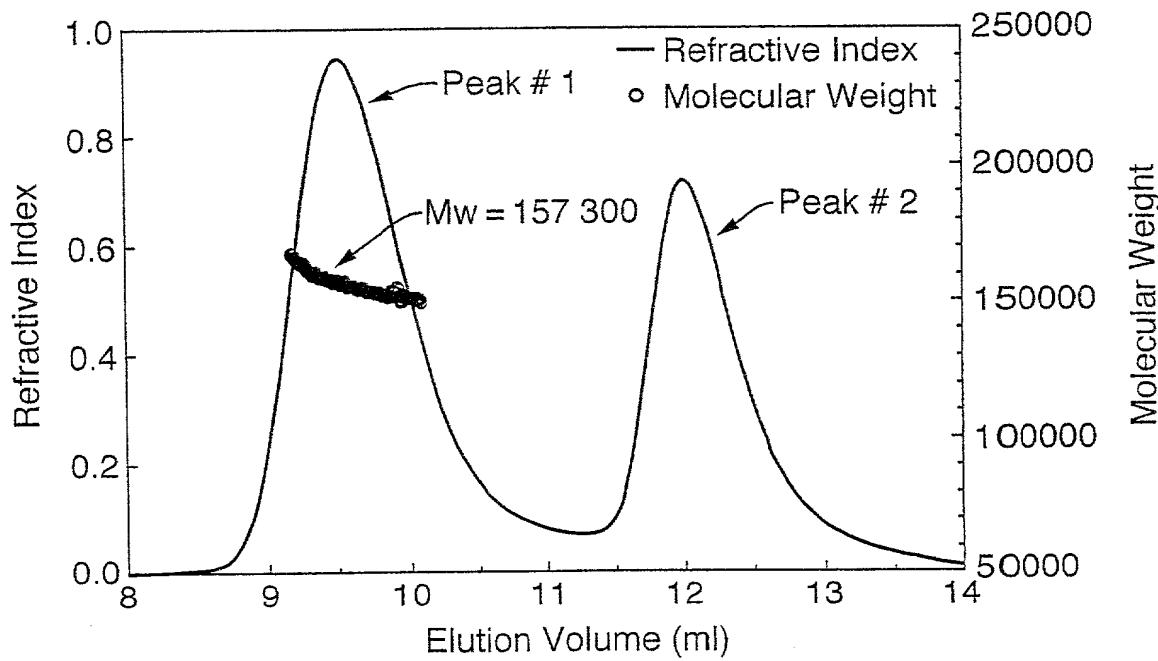


Fig.33.





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Fig.34.

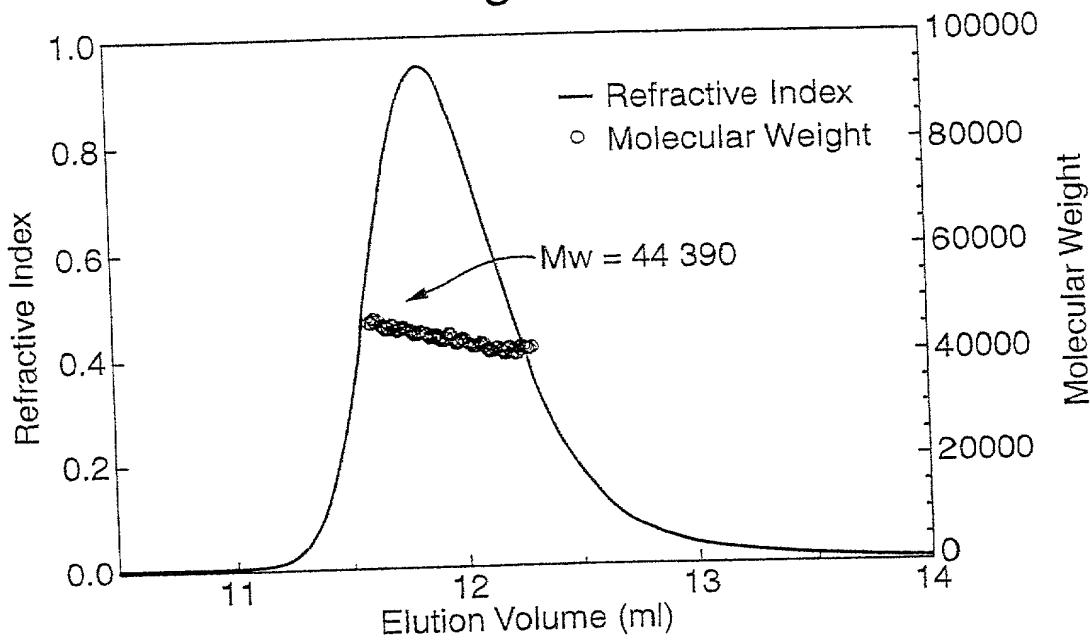


Fig.35.

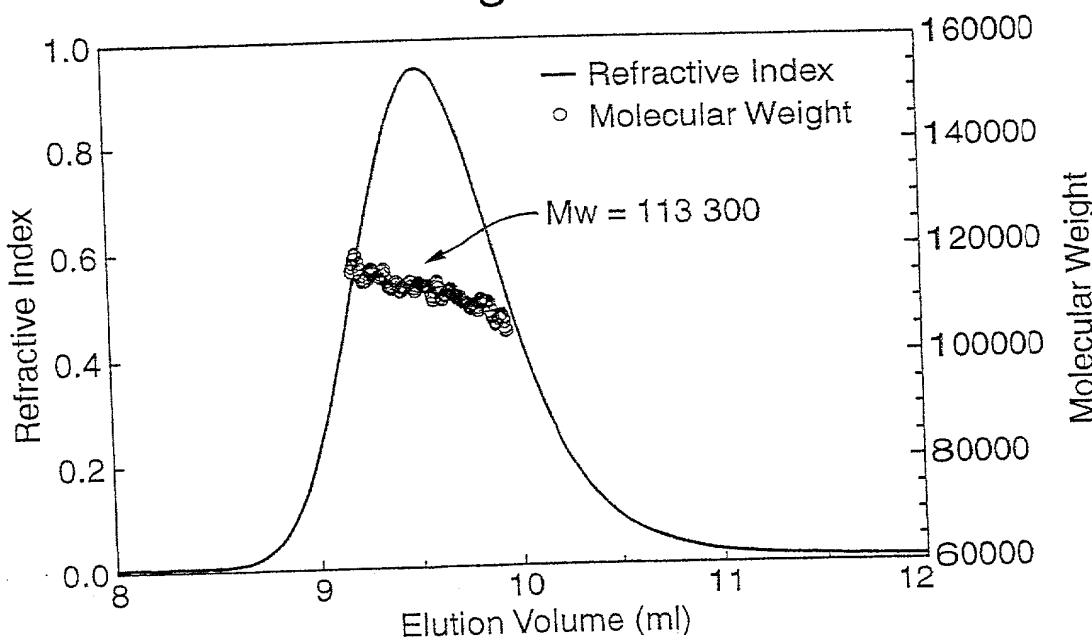
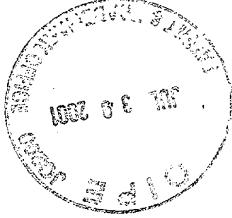


Fig. 36.

50 GRPFVEMYSEPEWIMTEGRELVIPPCRVTSPNITVTLKKFPLDTLIPDG
100 KRIIWDSRKGFISNATYKEIGLLTCATVNGHLYKTKNYLTHRQTNID
150 VVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHHQHKKLVNR
200 DLKTRQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVH
250 EKGPGDKTHICPPCPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVD
300 VSHEDPEVKFNWYVDGVEVHNAAKTKPREEQYNSTYRVVSVLTVLHQDWLN
350 GKEYKCKVSNKALPAPIEKTISAKGQPREPQVYTLPPSRDELTKNQVSL
400 TCLVKGFYPSDIAVEWESNGQPENN YKTTTPVLDSDGSFFLYSKLTVDKS
RWQQGNVFSCSVMHEALHNHYTQKSLSSLSPGK





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Fig.37.

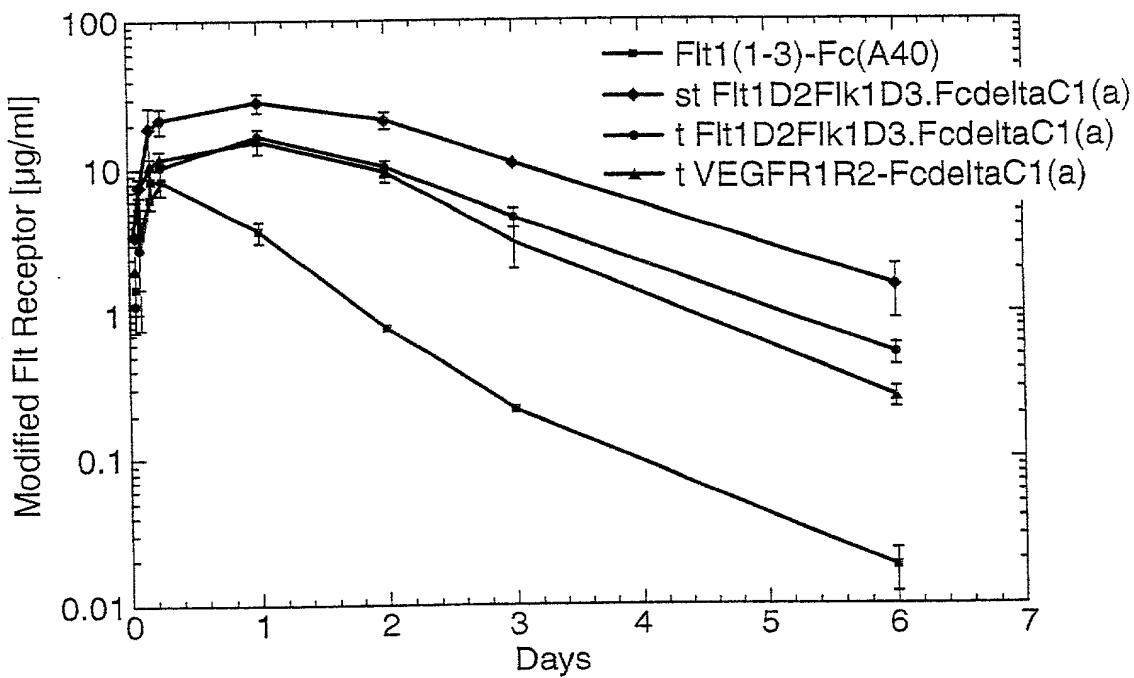


Fig.38.

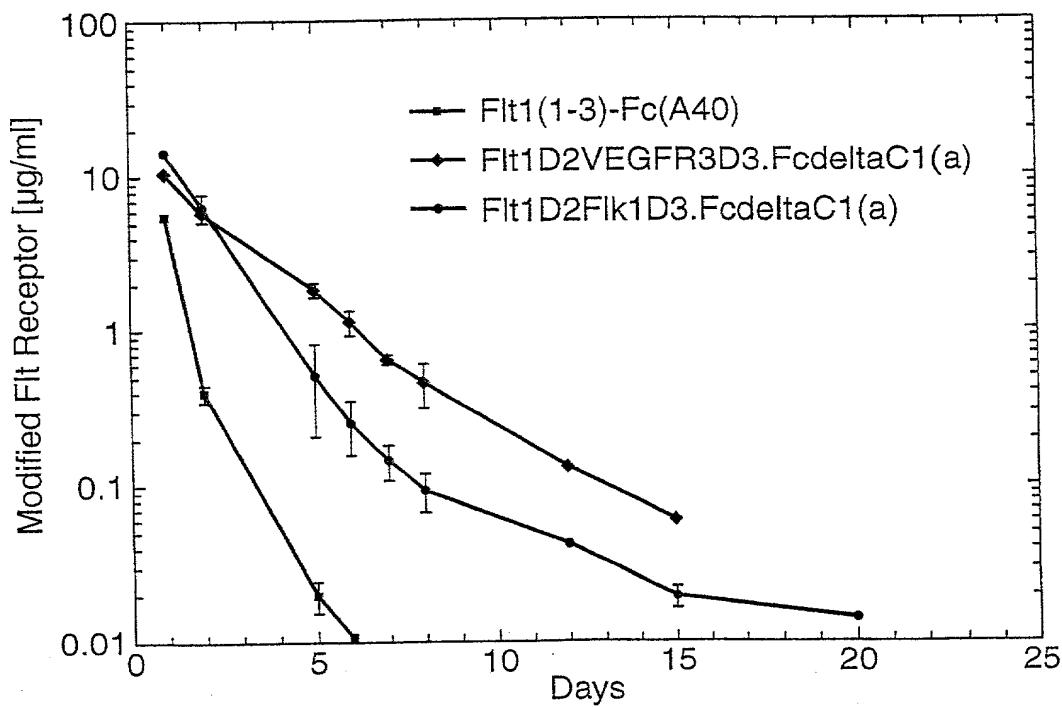




Fig.39.

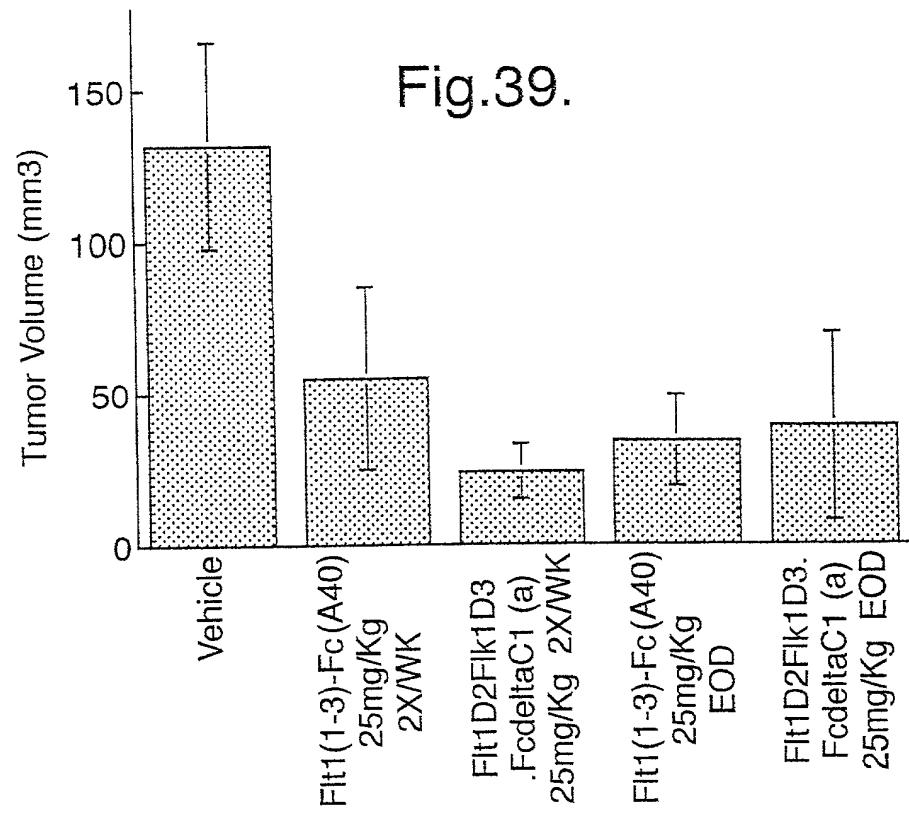


Fig.40.

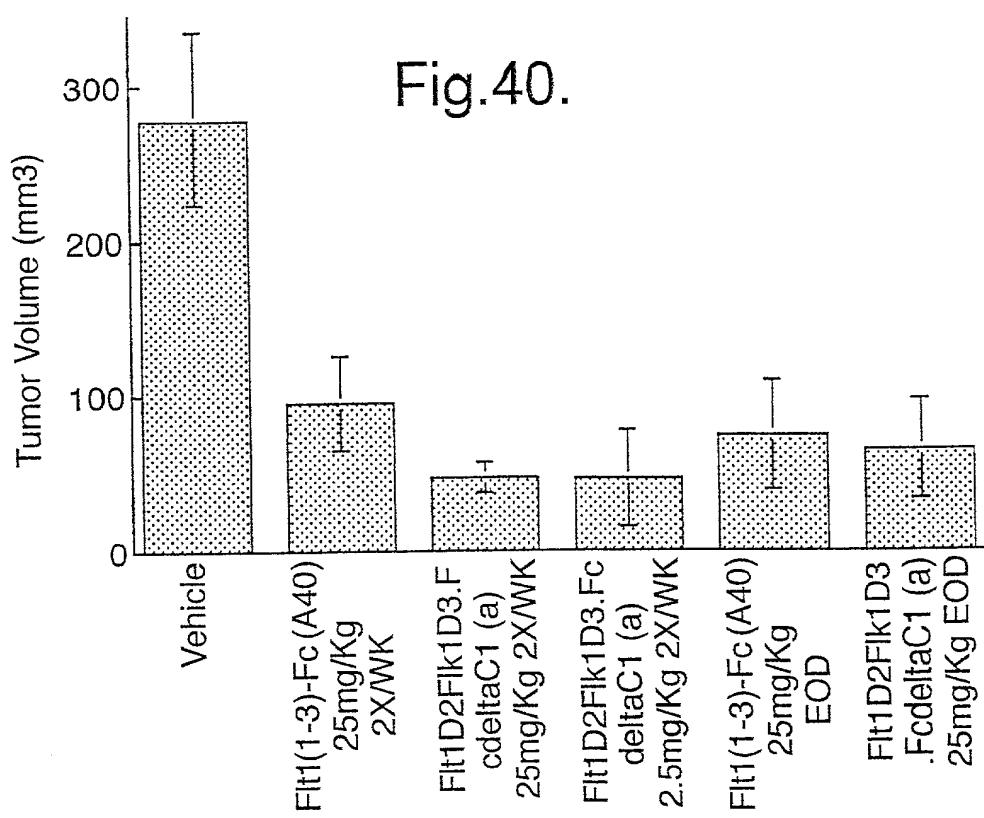
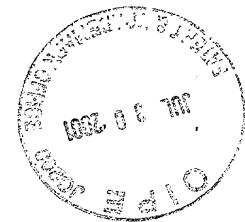
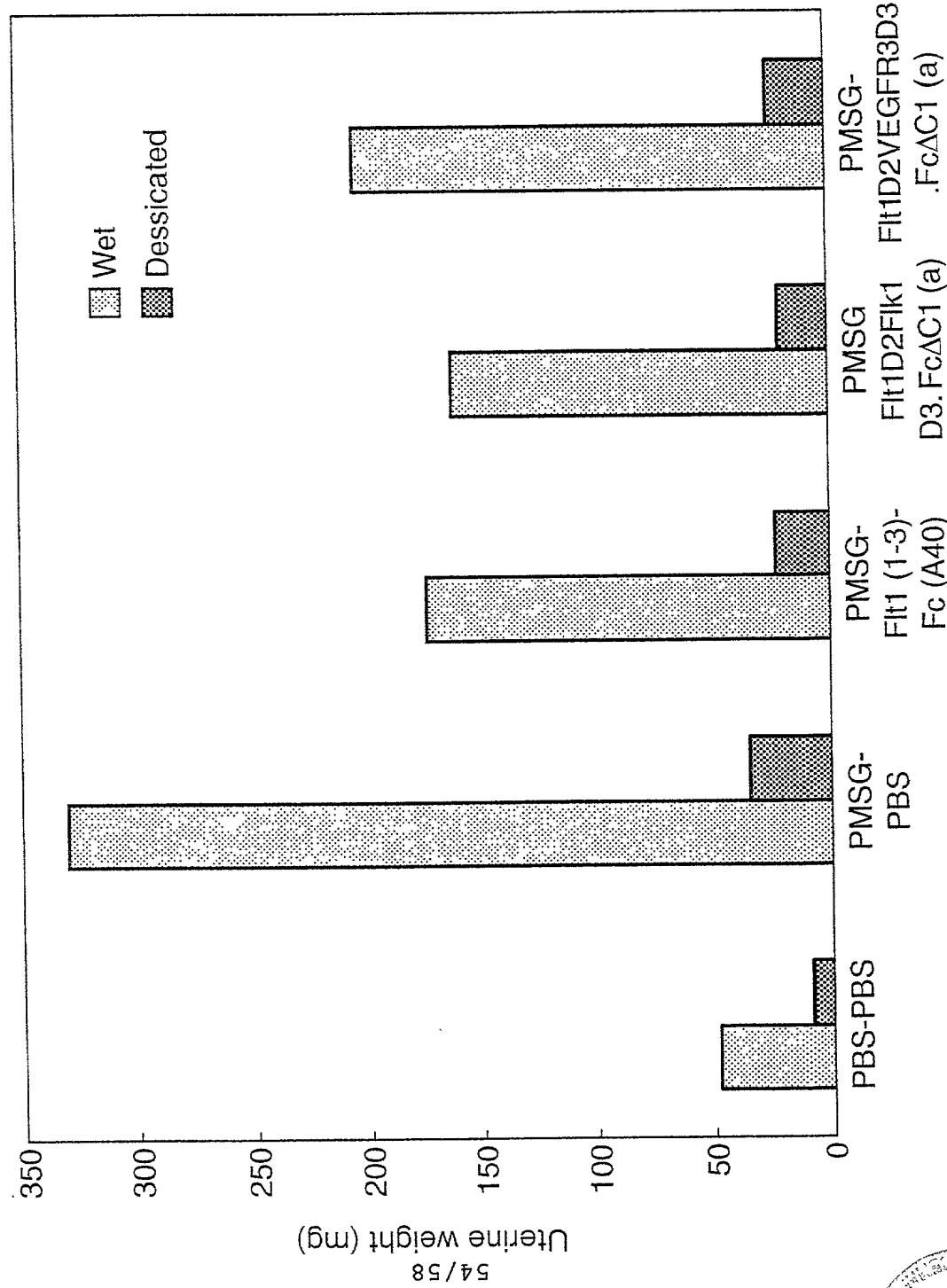


Fig.41.





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Fig.42A.

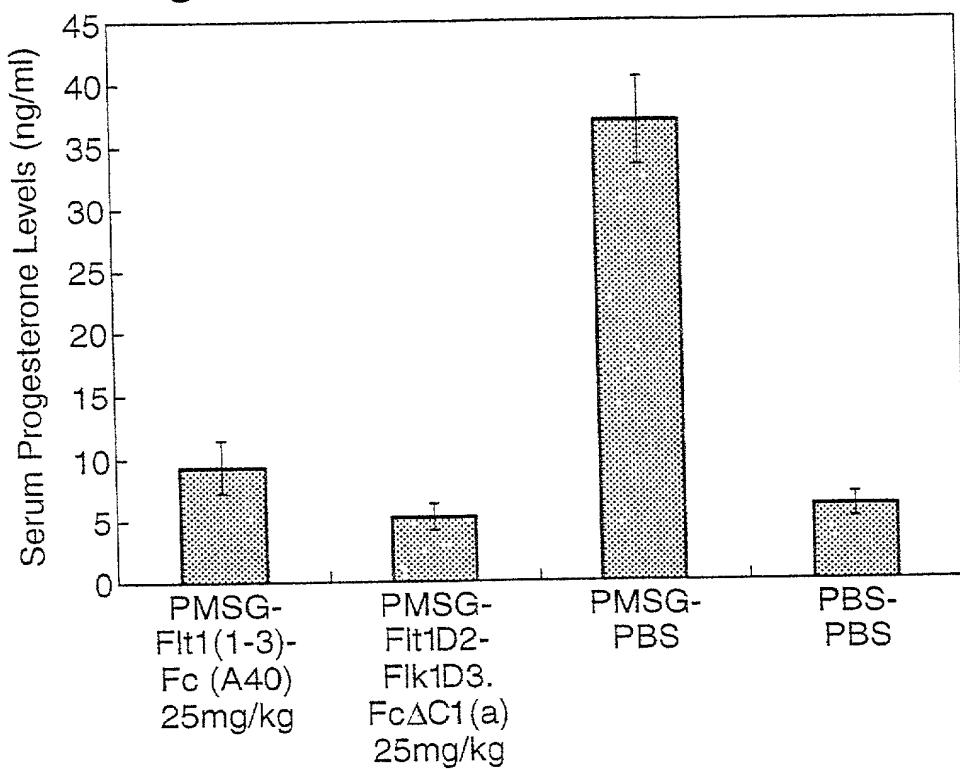


Fig.42B.

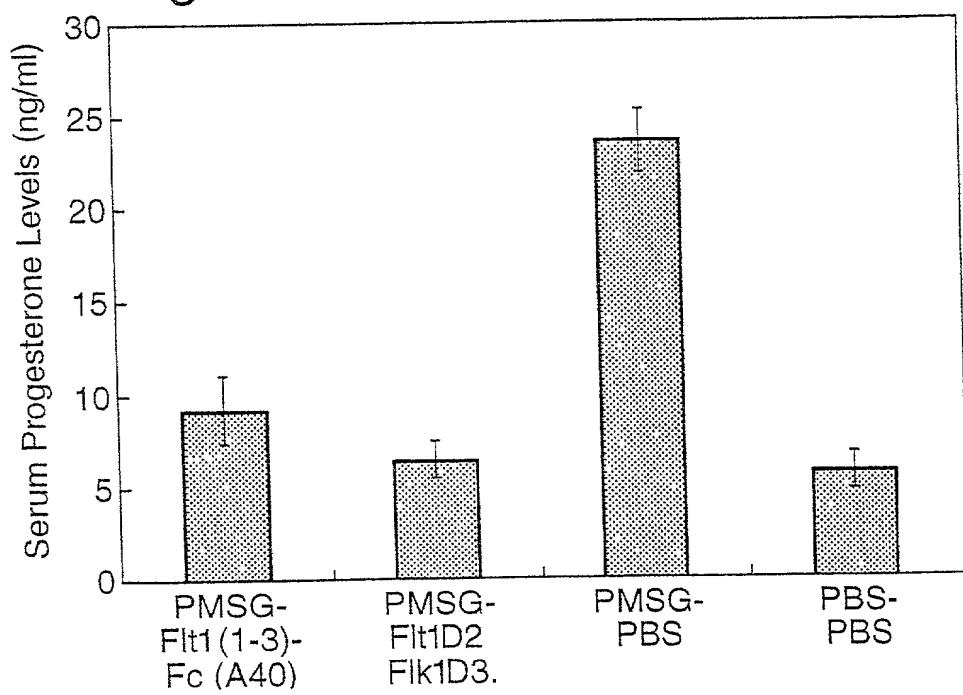
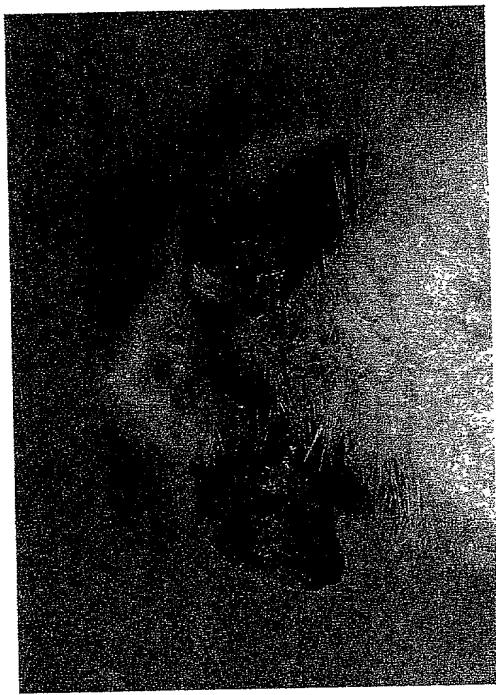


Fig.43



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Fig.44C



Fig.44B



Fig.44A

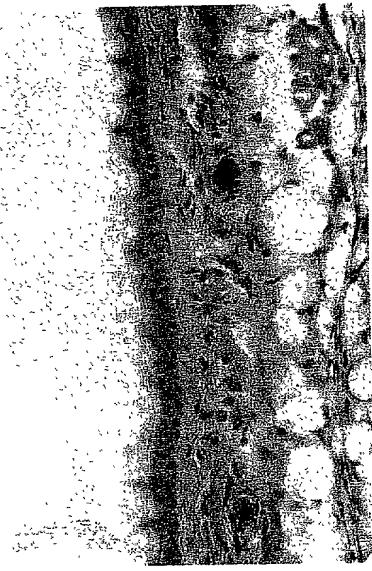


Fig.45

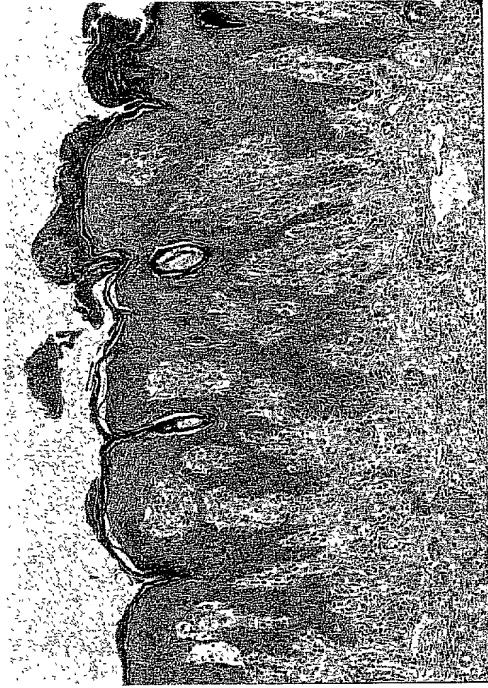


Fig.46 A-B

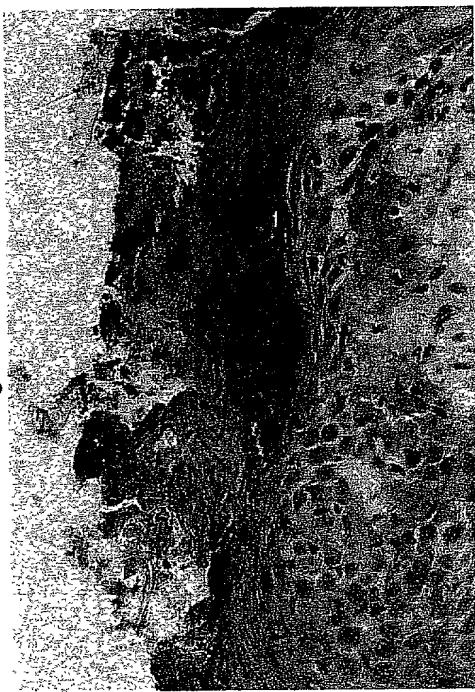


Fig.46B

